

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number:106579

TO: James Schultz

Location: cm1/12e18/11e12

Art Unit: 1635

Wednesday, October 29, 2003

Case Serial Number: 09331204

From: Toby Port

Location: Biotech-Chem Library

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Schultz,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port





STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Vo.	untary Results Feedback Form														
· >	I am an examiner in Workgroup: Example: 1610														
>	> Relevant prior art found, search results used as follows:														
	☐ 102 rejection														
	☐ 103 rejection														
	☐ Cited as being of interest.														
	☐ Helped examiner better understand the invention.														
	☐ Helped examiner better understand the state of the art in their technology.														
	Types of relevant prior art found:														
	☐ Foreign Patent(s)														
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)														
4	Relevant prior art not found:														
	Results verified the lack of relevant prior art (helped determine patentability).														
	Results were not useful in determining patentability or understanding the invention.														
Coı	nments:														

Desk. or sand completed forms to STED obsolvent Cham Whitery GM1 = Chc. Desk



STIC-Biotech/ChemLib

106579

From:

Schultz, James

Sent: To: Thursday, October 23, 2003 9:39 AM

STIC-Biotech/ChemLib

Subject: Seq Search request 09/331,204

Hello,

Could you please perform a length limited nucleotide sequence search against SEQ ID NOS: 4-8 and 13 in the above entitled application, where the maximum size of the returned hit is no longer than 22 nucleotides? SEQ ID NOS: 4, 5, 7, and 8 are 18mers, SEQ ID NO: 6 is a 21mer, and SEQ ID NO: 13 is a 12mer. This application recited multiple sequences as originally filed, before we started restricting to one sequence. Also, I need the <u>interference databases</u> searched.

Thanks, Doug Schultz

J. Douglas Schultz, Ph.D. AU 1635 (Biotechnology) Patent Examiner United States Patent and Trademark Office (703) 308-9355 (703) 746-3973 (fax) Office: CM1 12E18 Mail: CM1 11E12

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online times

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (whe	re applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	

44444 44444 44444 44444

Sequence 86378; Sequence 58852; Sequence 5725, Assequence 5725, Assequence 5715, Assequence 5715, Assequence 57556; Sequence 57556; Assequence 57535; Sequence 57535; Sequence

/ fg

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Sequence 14447, Application PC/TUS0238216
Sequence 14447, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENER AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NOMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSO ID NOS: 86841
SSO ID NO 41647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38943, Application PC/TUS0238216
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
SOFTWARE: Patentin version 3.2
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PCT-US02-38216-51896
PCT-US02-38216-86378
PCT-US02-38216-86378
PCT-US02-38216-57248
US-10-669-841-4725
US-10-669-841-5016
US-10-669-841-5016
PCT-US02-38216-70363
PCT-US02-38216-70363
PCT-US02-38216-70363
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PCT-US02-38216-70363
PCT-US02-38216-70363
PCT-US02-38216-9675
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Best Local Similarity 93.8
Matches 15, Conservative
      , TYPE: DNA
, ORGANISM: Homo sapiens
PCT-US02-38216-41647
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ORGANISM: Homo sapiens
PCT-US02-38216-38943
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LENGTH: 19
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                                                                                                October 27, 2003, 11:09:34 ; Search time 307.029 Seconds (without alignments) 97.777 Million cell updates/sec
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Sequence 2
Sequence 4
Sequence 2
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Sequence
Sequence
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(cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*

(cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*

(cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

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(cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*
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(c) 1993 - 2003 Compugen Ltd.
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PCT US02 38216 - 42689
PCT US02 - 38216 - 42141
PCT US02 - 38216 - 27376
PCT US02 - 38216 - 27376
PCT US02 - 38216 - 47426
PCT US02 - 38216 - 1818
PCT US02 - 38216 - 1818
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PCT-US02-38216-79761
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US-09-978-333C-2
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Maximum Match 100%
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Sequence 23360, Application PC/TUS0238216
SGNERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSCQ ID NOS: 86841
SSCQ ID NO 27360
LENGTH: 19
                                                                                                                                                                                                                                                                                                                            Sequence 27376, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REPERENCE: 55002
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOUTHARE: Patentin version 3.2
SEQ ID NO 27376
LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BIOINFORMATICALLY
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Pred. No. 1.4e+04;
0; Mismatches 0; Indels
                                                                                       Query Match 80.0%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 1;
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Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
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PCT-US02-38216-27360
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-42141
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Best Local Similarity
Matches 14; Conserv
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PCT-US02-38216-27376
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PCT-US02-38216-18278
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PCT-USO2-38216-42141
PCT-USO2-38216
Sequence 42141, Application PC/TUSO238216
Sequence 42141, Application PC/TUSO238216
GENERAL INFORMATION:
APPLICANT: Roselta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENERS AND USES THEREOF
TITLE OF INVENTION: GENERS AND USES THEREOF
CURRENT APPLICATION NUMBER: PCT/USO2/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSEQ ID NO 42141
LENGTH: 22
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GENERAL INFORMATION:
APPLICANT: ROSECTA Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
                                                                                                                              CT-0502-38216-46976
Sequence 46976
Application PC/TUS0238216
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 5502
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT PILING DATE: 2002-11-12
SOFTWARE: Patentin version 3.2
SEQ ID NO 46976
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CORGANISM: Homo sapiens
PCT-US02-38216-26689
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; ORGANISM: Homo sapiens
PCT-US02-38216-46976
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Matches 15; Conserv
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LENGTH: 22
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Sequence 18418, Application PC/TUS0238216
| Sequence 18418, Application PC/TUS0238216
| GENERAL INFORMATION:
| APPLICANT: Rosetta Genomics LTD |
| TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY |
| TITLE OF INVENTION: GENES AND USES THEREOF |
| FILE REFRENCE: 55002 |
| CURRENT APPLICATION NUMBER: PCT/US02/38216 |
| CURRENT FILING DATE: 2002-11-12 |
| NUMBER OF SEQ ID NOS: 96841 |
| SSOTWARE: Patentin version 3.2 |
| SSO ID NO 19418 |
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GENERAL INFORMATION.
FAPPLICANT: Roselta Genomics LTD
TITLE OF INVENTION.
FILE REPERBNCE: 5502
CURRENT APPLICATION UNDER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSEQ ID NO 39237
LENGTH: 20
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PCT-US02-38216-51847
PCT-US02-38216
Sequence 51847, Application PC/TUS0238216
GENERAL INFORMATION
APPLICANT: ROSetta Genomics LTD
APPLICANT: ROSetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TILE REFERENCE: 55002
FILE REFERENCE: 2002-11-12
CURRENT PALLICA DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSEQ ID NOS: 86841
SSEQ ID NO 51847
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 1;
Pred. No. 1.7e+04;
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Best Local Similarity 88.2
Matches 15; Conservative
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) ORGANISM: Homo sapiens
PCT-US02-38216-18418
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CRGANISM: Homo sapiens
PCT-US02-38216-39237
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PCT-US02-38216-51847
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
GENERAL SOCIETA GENDING LTD
TITLE OF INVENTION:
GENERAL SOCIETA
TITLE OF INVENTION:
GENES AND USES THEREOF
TITLE OF INVENTION:
GENES AND USES THEREOF
CURRENT FILING DATE:
2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PACENTIN VERSION 3.2
SEQ ID NO 61865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 47426, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: ROSetta Genomics LTD
TILE OF INVENTION: BLOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TILLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.7%; Score 13.8; DB 1; Length 19; Best Local Similarity 88.2%; Pred. No. 1.7e+04; Matches 15; Conservative 0; Mismatches 2; Indels
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       GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF FILE REFRENCE: 55002 CURRENT APPLICATION NUMBER: PCT/USO2/38216 CURRENT FILING DATE: 2002-11-12 NUMBER OF SEQ ID NOS: 86841 SOFTWARE: Patentin version 3.2 SEQ ID NO 19278
                                                                                                                                                                                                                                                                                                                                                                                  1 TTGGAGGGGTGGTGGG 17
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Best Local Similarity 88.2
Matches 15, Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-61865
                                                                                                                                                                                                               ) ORGANISM: Homo sapiens
PCT-US02-38216-18278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
PCT-US02-38216-47426
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LENGTH: 19
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Sequence 75562, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT Resetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICALION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 75562
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63940, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Reserta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 5502
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 22
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Query Match
76.7%; Score 13.8; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels
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76.7%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2;
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CORGANISM: Homo sapiens
PCT-US02-38216-63940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-75562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
PCT-US02-38216-63940
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PCT-US02-38216-75562
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Search completed: October 27, 2003, 18:22:55 Job time : 308.029 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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No.
                                      // Search time 2356.29 Seconds
(without alignments)
253.343 Million cell updates/sec
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   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                       33363688 seqs, 16581889874 residues
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first 45 summaries
                           nucleic search, using sw model
                                       October 27, 2003, 10:32:35
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                                                              US-09-331-204A-4
18
1 ttggagggggtggtggggg
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Maximum Match 100
                                                                                                                              length: 0
length: 22
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Perfect score:
Sequence:
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cgn2_6/ptodata/1/pna/US6013_COMB.seq:
cgn2_6/ptodata/1/pna/US6013_COMB
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Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 17, Appl

US-08-387-041A-3 US-09-331-204-1 US-09-331-204A-4 US-09-786-436-17

3000

28

Description

SUMMARIES

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8250-011
      TELECOMMUNICATION INFORMATION:
TELEPAX: 415-854-366
TELEPAX: 415-854-3694
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 18, Conservative
                                                                                                                              US-08-387-041A-3
                                                                                                                                                                                                                                                            US-09-331-204-1
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                   CORRESPONDED:
ADDRESSEE: Pennace
ADDRESSEE: Attention of the ...
GTREET: 1155 Avenue of the ...
CITY: New York
COUNTY: New York
COUNTY: United States of America
ID 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,041A
FILING DATE: 02-FEB-1995
FILING DATE: 02-FEB-1995
                 9 US-09-331-2044-6
9 US-09-331-2044-6
9 US-09-331-2044-6
9 US-09-331-2044-8
9 US-09-331-2044-8
9 US-09-331-2044-8
9 US-09-331-2044-4
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0 US-08-472-801-2663
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0 US-10-310-188-338-2663
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US-09-331-204A-4

US-09-331-204A-4

Sequence 4, Application US/09331204A

Sequence 4, Application US/09331204A

GENERAL INFORMATION:
APPLICANT: Tam, Robert
APPLICANT: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT PILING DATE: 1999-08-20
FRICH APPLICATION NUMBER: DET/US97/23927
FRICH APPLICANTON NUMBER: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Tan. Robert.
TITLE OF INVENTION: INMUNE RESPONSE
TITLE OF INVENTION: INMUNE RESPONSE
FILE REPREBRIES: IONSEQUENCE
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT APPLICATION NUMBER: PCT/US97/23927
FRIOR APPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID NOS: 6
SEGVEMBER: PATCH IN VOICE: 2.0
SEQ ID NO: 1
LENGTH: 18
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 18; DB 19;
100.0%; Pred. No. 4.8e+03;
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LENGTH: 18 base pairs
TYPE: nucleic acid
STRNDEDDENESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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ORGANISM: Artificial Sequence
FEATURE:
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Sequence 6, Application US/09331204
GENERAL INFORMATION:
APPLICANT: Tam. Robert
TITLE OF INVENTION: GRICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REPREBENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
FRIOR PLICATION NUMBER: PCT/US97/23927
FRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                                                        Sequence 4, Application US/08387041A
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
TITLE OF INVENTION: OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
COMPUTER: EN PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 02-FEB-1995
CLASSIFICATION S14
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET WUMBER: 25,227
REFERENCE/DOCKET WUMBER: 25,227
REFERENCE/DOCKET WUMBER: 8250-011
TELEPHONE: 415-854.3660
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100.0%; Pred. No. 4.8e+03
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                                                                                                                                                                                                                                                                                                                                                                         CITY: New Join.
STATE: New York
COUNTRY: United States of America
ZIP: 10036
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                                                          18 TTGGAGGGGGTGGGG 1
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Best Local Similarity 100.0
Matches 18; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415-854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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US-09-331-204-6
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LENGTH: 21
TYPE: DNA
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                                                                                    Query Match
100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred, No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Inform, Hermann
APPLICANT: Inford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Morif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: Clo41/7010 (AMS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09786436
GENERAL INFORMATION:
APPLICANT: Wagner, Hermann
APPLICANT: Lipbord, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses;
TITLE OF INVENTION: Thereof
FILE REFERENCE: C1041/7010 (AWS);
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Score 18; DB 33;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0;
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US-09-786-436-17
Sequence 17, Application US/09786436
GENERAL INFORMATION
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; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 18; Conservative
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US-09-786-436-42/c
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Sequence 7, Application US/09331204A
GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tam, Robert
ITTLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resj
FILE REFERRINCE: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEC ID NOS: 28
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                         Sequence 8, Application Us/09331204A
GENERAL INFORMATION:
APPLICANT: ICH Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
ITILE OF INVENTION:
FILE REFERENCE: 215/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILE OF INVENTION:
PRIOR PPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 19997-12-19
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216/013-US1
       Gaps
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       Indels
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Pred. No. 1.9e+04;
0; Mismatches 1;
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Pred. No. 7.8e+04;
0; Mismatches 2;
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       Mismatches
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GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo AppreNIE REFERENCE: 216/013-US1
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88.9%;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity 88.99
    17, Conservative
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SOFTWARE: Patentin v
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US-09-331-204A-8
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US-09-331-204A-9
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LENGTH: 18
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    Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ITCM: Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION:
G-rich Oligo Aptamers and Methods of Modulating an Immune Responsible of Invention Windholds:
TITLE OF INVENTION:
GURRENT APPLICATION WINDHER: US/09/331,204A
CURRENT APPLICATION WINDHER: PCT/US97/23927
PRIOR PRILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
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APPLICANT: Tam, Robert

ITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN

ITLE OF INVENTION: IMMUNE RESPONSE

FILE REPERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204

CURRENT APPLICATION NUMBER: US/09/331,204

CURRENT APPLICATION NUMBER: D99-08-20

PRIOR RILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 6

SCOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 5

LENGTH: 18
                      ) OTHER INFORMATION: Description of Artificial Sequence: An oligomer of OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic of OTHER INFORMATION: acid. This term includes oligomers consisting of OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-6
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100.0%; Score 18; DB 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: synthetic construct US-09-331-204A-6
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LENGTH: 21
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Score 16.4; DB 19; Length 18; Pred. No. 1.9e+04;

91.1%; 94.4%;

Query Match Best Local Similarity

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us-09-331-204a-4.szlm22.rnpm

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US-10-188-38943

VS-10-110-188-38943

Sequence 38943, Application US/10310188

Sequence 38943, Application US/10310188

GENERAL INFORMATION:
APPLICANT: ROSettademonics
TITLE OF INVENTION: USES THEREOF
FILE REPRENCE: 47487

CURRENT APPLICATION WHORE: US/10/310,188

CURRENT APPLICATION WHORE: US/10/310,188

CURRENT APPLICATION NOS: 86841

NUMBER OF SEQ ID NOS: 86841
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          Length 18;
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Pred. No. 1.1e+05;
0; Mismatches 1; Indels
          80.0%; Score 14.4; DB 50;
llarity 93.8%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 1;
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                                                                                                        3 GGAGGGGGTGGTGGGG 18
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Best Local Similarity 93.8%;
Matches 15; Conservative (
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; ORGANISM: Homo sapiens
US-10-310-188-38943
                                 Best Local Similarity
Matches 15; Conserv
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LENGTH: 19
            Query Match
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REPERBNCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT PILING DATE: 2002-12-19
NUMBER OF SOL ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 41647
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APPLICANT: Tam, Robert
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: G-RICHARD RESPONSE
FILE REFERENCE: 1000-80-20
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1997-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR TILING DATE: 1997-12-19
SOFTWARE OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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82.2%; Score 14.8; DB 19; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 2; Indels (
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88.9%; Pred. No. 7.8e+04;
tive 0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-331-204-4; Sequence 4, Application US/09331204; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          1 TTGGAGGGGGTGGTGGGG 18
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                              ) TYPE: DNA

) ORGANISM: synthetic construct

US-09-331-204A-9
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Best Local Similarity 88.9
Matches 16; Conservative
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CORGANISM: Homo sapiens
US-10-310-188-41647
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Sequence 4, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 26, Appl
Sequence 36, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 52, Appl
Sequence 1934, Appl
Sequence 1936, Appl
Sequence 1936, Appl
Sequence 1936, Appl
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Sequence 67, Appl
Sequence 67, Appl
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US-09-84-162A-22/C
| US-09-84-162A-22/C
| Sequence 22, Application US/09874162A
| Patent No. US20020155452A1
| GENERAL INFORMATION:
| APPLICANT: Kontz, Jason
| APPLICANT: Kontz, Jason
| TITLE OF INVENTION: FUSION OF JAZF1 AND JJAZ1 GENES IN
| TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
| FILE REFERENCE: 05311-024001
| CURRENT FILING DATE: 2001-06-04
| PRIOR APPLICATION NUMBER: US/09/874,162A
| PRIOR FILING DATE: 2000-06-02
| NUMBER OF SEQ ID NOS: 23
| SOFTWARE: FastSEQ for Windows Version 4.0
1 US-09-988-115A-22

2 US-10-125-585-5333

US-10-126-460-4

US-10-126-460-4

US-10-126-460-4

US-09-854-883-174

US-09-854-883-174

US-09-757-004-110

US-09-828-034-31

US-09-848-0338-117

US-10-06-06-0694-117
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Pred. No. 1.3e+04;
0; Mismatches 1;
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US-09-740-332-2132/c
; Sequence 2132, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
// OTHER INFORMATION: primer for PCR US-09-874-162A-22
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Best Local Similarity 93.3%;
Matches 14; Conservative 0
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ORGANISM: Artificial Sequence
         GGAGGGGGTGGTGGG 17
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2132, Ap
2133, Ap
2422, Ap
2423, Ap
2133, Ap
2423, Ap
2422, Ap
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30, Appl
26, Appl
35, Appl
3, Appli
13, Appli
20, Appl
                                                                                                                                                     October 27, 2003, 11:25:34; Search time 387.943 Seconds (without alignments) 124.432 Million cell updates/sec
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Sequence
Sequence
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/ GGDZ_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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/ GGDZ_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ GGDZ_6/ptodata/1/pubpna/USO0NEW_PUB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-740-332-2132
US-09-740-332-2133
US-09-740-332-2423
US-09-740-332-2423
US-09-817-879-2132
US-09-817-879-2133
US-09-817-879-2422
US-09-817-879-2422
US-10-059-877-26
US-10-059-877-26
US-10-108-108A-35
US-10-108-108A-35
US-10-108-846-35
US-09-988-115A-31
US-09-988-115A-31
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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18
1 ttggagggatgatc
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Match Length
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length: 22
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Maximum DB seq
                                                                                                                                                                                                                                                 Title:
Perfect score:
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Sequence 2132, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
APPLICAMY: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relair TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: MHH800-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Bazymatic Nucleic Acid Treatment of Diseases or Conditions Relat
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2423
LENGTH: 17
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Pred. No. 2e+04;
2; Mismatches 0; Indels
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Pred. No. 2e+04;
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LOCATION:
OTHER INFORMATION: oligonucleotide substrate
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CTHER INFORMATION: Oligonucleotide substrate
US-09-740-332-2423
                                                                                                                               ) OTHER INFORMATION: oligonucleotide substrate US-09-740-332-2422
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                                 ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: artificial sequence
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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LOCATION:
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US-09-817-879-2132/c
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LENGTH: 17
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Publication No. US20030125270A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9422
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2133, Application US/09740332
Publication No. US20030125270A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Braymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C virus Infection
FILE REPERBNCE: RP1 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
FROID NO 2133
FROID NO 2133
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERROR: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                   72.2%; Score 13; DB 11; Length 17; 100.0%; Pred. No. 2e+04; Antive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Oligonucleotide substrate US-09-740-332-2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: oligonucleotide substrate US-09-740-332-2133
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                                                                                                                                                                                                                                                  ORGANISM: artificial sequence
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NAME/KEY: misc_feature
LOCATION:
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Best Local Similarity
Matches 13; Conserv
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US-09-740-332-2133/c
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Sequence 26, Application US/10059877

Sequence 26, Application US/20030157490A1

Sequence 26, Application Work US20030157490A1

Sequence 26, Application Work US20030157490A1

SEDERAL INFORMATION:

APPLICANT: CHAO, ULEE

APPLICANT: CHAO, ULLE

TITLE OF INVENTION: HYPERTENSION

FILE REFERENCE: 19113.008102

CURRENT APPLICATION NUMBER: US/10/059,877

CURRENT APPLICATION NUMBER: 09/495,140

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 1999-09-03

PRIOR FILING DATE: 1999-09-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03
                        Sequence 2423, Application US/09817879
Sequence 2423, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: MRHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 2423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490Ale; OTHER INFORMATION: synthetic construct
US-10-059-877-26
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Pred. No. 2e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGGGGGGGGGGGG 16
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Best Local Similarity 84.0.
Thes 11; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
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NAME/KEY: misc_feature
LOCATION:
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US-10-303-109A-30/c
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US-09-817-879-2133/C
Sequence 2133, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
Publication No. US20030171311A1
GENERAL INFORMATION:
PAPPLICATON: Floozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
SOFTWARE: Patentin version 3.0
SEQ ID NO 2133
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Publication No. US20030171311A1
GENERAL INFORMATION:
THE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION WHERE: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
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Pred. No. 2e+04;
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                                    Indels
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   Pred. No. 2e+04;
; Mismatches 0;
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COTHER INFORMATION: oligonucleotide substrate US-09-817-879-2133
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72.2%; Scc
Best Local Similarity 100.0%; Pr
Matches 13; Conservative 0;
Best Local Similarity 100.0%; P
Matches 13; Conservative 0;
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ORGANISM: artificial sequence
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US-09-817-879-2422
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LENGTH: 17
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APPLICANT: Goldsby, Richard A.
APPLICANT: Gridsby, Richard A.
APPLICANT: Ferguson, Stacy E.
APPLICANT: Kurciuson, Stacy E.
APPLICANT: Tomizuka, Yosuma
APPLICANT: Tomizuka, Yosuma
APPLICANT: Tomizuka, Sazuma
APPLICANT: Tomizuka, Sazuma
APPLICANT: Tomizuka, Sazuma
APPLICANT: Tomizuka, Sazuma
APPLICANT: Tomizuka, Yosuma
APPLICANT: Stacy
INTILE OF INVENTION: Expression of Xenogenous (Human)
IITLE OF INVENTION: Expression of Xenogenous (Human)
CURRENT APPLICATION NUMBER: US/09/988,115A
CURRENT FILING DATE: 2002-08-09
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0
                                     APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE RTSP-0.36

CURRENT APPLICATION NUMBER: US/10/181,846

CURRENT FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: PCT/US01/01416

PRIOR APPLICATION NUMBER: 09/490,692

PRIOR APPLICATION NUMBER: 09/490,692

PRIOR FILING DATE: 2000-01-24

NUMBER OF SEQ ID NOS: 176

LENGTH: 20
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87.5%; Pred. No. 2.3e+04;
tive 0; Mismatches 2;
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US-10-181-846-35
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PRIOR FILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 60/16,410
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SCOTTWARE: 22
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, Sequence 3, Application US/09989115A
; Publication No. US20030037347A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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                    APPLICANT: Nicholas M. Dean
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Matches 14; Conservative
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JOHNSTON CHAOL LEE
APPLICANT: CHAOL JULE
APPLICANT: CHAOL JULIE
APPLICANT: CHAOL TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
TITLE OF INVENTION: 1013.008102
CURRENT APPLICATION NUMBER: US/10/059,888
CURRENT APPLICATION NUMBER: 09/495,140
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 08/856,141
SPRIOR FILING DATE: 1999-09-03
PRIOR SEQ ID NOS: 31
SEQ ID NO 26
FRANCE: FASELES FOR WINDOWS VETSION 4.0
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Sequence 30, Application US/10303109A
Publication No US20030194726A1
GENERAL INPORMATION:
APPLICANT: BOLCHAKOVA, Elena
APPLICANT: ROZZELLE, James
TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
FILE REFERENCE: 477702
CURRENT APPLICATION NUMBER: US/10/303,109A
CURRENT APPLICATION NUMBER: US 60/334,798
PRIOR APPLICATION NUMBER: US 60/334,798
PRIOR FILING DATE: 200111-30
NUMBER OF SEQ 1D NOS: 39
SOFTWARE: Patentin version 3:2
LENGTH: 17
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Pest Local Similarity 87.5%; Pr. Matches 14; Conservative 0;
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US-10-059-888-26
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RESULT 15 US-09-988-115A-13/c

Sequence 35, Application US/10181846 Publication No. US20030083297A1 GENERAL INFORMATION:

RESULT 13 US-10-181-846-35

Search completed: October 27, 2003, 19:00:52 Job time: 387.943 secs

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Sequence 3
Sequence 3
Sequence 5
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Patent No. 5932556
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                US-08 486-513-2
US-08 486-513-2
US-08 486-535-2
US-08 486-536-2
US-08 486-536-2
US-08 486-536-2
US-08 486-513-3
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/POCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHARS: 714-525-3433
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STRET: 3000 CITY: La Habra
STATE: California
COUNTRY: United States of America
71P: 90831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Crockett & Fish
3000 S. Augusta Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trockedectected
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: __nucleic acid
Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nuclei
STRANDEDNESS:
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RESULT
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Sequence 13, Sequence 4, Al
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Sequence 4, 7
Sequence 4, 7
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1: / GGTZ = 6/ptodata/1/ina/5A_COMB.seq:*
1: / GGTZ = 6/ptodata/1/ina/5B_COMB.seq:*
3: / CGTZ = 6/ptodata/1/ina/6A_COMB.seq:*
4: / CGTZ = 6/ptodata/1/ina/6B_COMB.seq:*
5: / CGTZ = 6/ptodata/1/ina/PCTUS COMB.seq:*
6: / CGTZ = 6/ptodata/1/ina/PCTUS COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-529-878B-44
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US-08-176-712-2
US-09-411-291-2
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PCT-US93-04754-13
PCT-US94-01235-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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length: 22
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Sequence:
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Maximum DB seq
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| Sequence 45, Application US/08529878B
| Patent No. 15928566|
| Patent No. 1592856|
| Patent No. 1592856|
| TILLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
| CORRESPONDENCES: 48
| COUNTY: La Habra
| STATE: 3000 S. Augusta Court |
| COUNTRY: United States of America
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFRENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3333
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
FILING DATE: 13-SEP-1995
CLASSIFICATION: 474
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NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
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) MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4
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SEQUENCE CHARACTERISTICS:
LENGTH 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: unknown
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TELEFAX: 714-525-3303
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US-08-529-878B-45
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                                            Sequence 44, Application US/08529878B
Sequence 44, Application US/08529878B
Sequence 44, Application US/08529878B
Setent NO. 5932556
SENERAL INFORMATION:
APPLICANT: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STREET: 000 S. Augusta Court
CITY: La Habra
COUNTRY: United States of America
ZIP: 90631
COMPUTER READABLE FORM: PC-DOS/MS-DOS
SOFTWARE: IBM PC compatible
COMPUTER READABLE FORM: PC-DOS/MS-DOS
SOFTWARE: MordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: NUMBER: 33,880
RESPERBACE/ORDET INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
RESPERBACE/ORDET NUMBER: 213/003
TELEPHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08529878B
Patent No. 5932566
GREAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSED: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
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100.0%; Score 18;
Best Local Similarity 100.0%; Pred. No. 3
Matches 18; Conservative 0; Mismatch
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TIGGAGGGGGTGGTGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-529-878B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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TOPOLOGY: unk
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TELEFAX: 71
TELEX:
                      RESULT 2
US-08-529-878B-44
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us-09-331-204a-4.szlm22.rni

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Sequence 26, Application US/09495140

Patent No. 6376182

GENERAL INFORMATION:

APPLICANT: CHAO, LEE

APPLICANT: CHAO, UTLE

APPLICANT: CHAO, UTLE

TITLE OF INVENTION:

TITLE OF INVENTION: TISSUE KALLIGREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT:

TITLE OF INVENTION: TISSUE KALLIGREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT:

TITLE OF INVENTION: 19113.0081

TITLE OF INVENTION: WHERE: US/09/495,140

CURRENT APPLICANTON NUMBER: 09/399,566

EARLIER PELICATION NUMBER: 09/399,566

EARLIER PELING DATE: 1999-09-03

SEALIER RILING DATE: 1999-09-03

SOFTWARE: Rabilicanton NUMBER: 08/856,141

EARLIER PELING DATE: 1997-05-14

NUMBER OF SEQ ID NOS: 31

SOFTWARE: RasiseQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 17
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OTHER INFORMATION: Description of Artificial Sequence:/No. 6376182e
CTHER INFORMATION: synthetic construct
US-09-495-140-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                        COUNTER TO A COUNTER TO A COUNTER TO A COUNTER TREADABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION COMPATION OF SYSTEM: PC-DOS/NS-DOS SOFTWARE: PATCHIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION DATA: PAPLICATION DATA: APPLICATION OF CLASSIFICATION: CURNOWN>
PRIOR APPLICATION OF COMPOSE: OF CLASSIFICATION: CURNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: PADES: PAPLICA ID: NUMBER: 31,284
REFERENCE/DOCKET WINDER: 31,284
REFERENCE/DOCKET WINDER: YU114
TELEPAK: (404)-873-8794
INFORMATION: COMPOSE: COMPOSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.8; DB 4; Length 17;
Pred. No. 3e+03;
0; Mismatches 2; Indels
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Pred. No. 1.7e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-411-291-2
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93.38;
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Best Local Similarity 87.5%;
Matches 14; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGAGGGGGTGGTGGG 17
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Best Local Similarity
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US-09-495-140-26
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                                                 Gaps
                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08476712
; Sequence 2, Application US/08476712
; Sequence 2, Application US/08476712
; Patent No. 5962426
; GENERAL INFORMATION:
    TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Patrea L. Pabst
    STREET: 2800 One Allantic Center STREET: 2800 One Allantic Center STREET: 2800 One Allantic Center STREET: 30309-3450
CONTYR: GA
    STREET: 1201 West Peachtree Street
    STREET: 1201 West Peachtree Street
    STREET: 2800 One Allantic Center STREET: 1201 West Peachtree Street
    STREET: 2800 One Allantic Center
    STREET: 1201 West Peachtree Street
    STREET: 30309-3450
COMPUTER: Toppy disk
    COMPUTER: Toppy disk
    SOFTWARE: Patentin Release #1.0, Version #1.25
    COMPUTER: Toppy disk: 105/08/476,712
    STATORNEY APPLICATION: 514
    ATTORNEY APELICATION: 514
    ATTORNEY AGENT INFORMATION: 514
    TELECOMMUNICATION INPORMATION: 7 TELECOMUNICATION INPORMATION: 7 TELECOMMUNICATION INPORMATION: 7 TELECOMMUNICATION: 7 TELECOMMUNICATION: 7 TELECOMMUNICATION: 7 TELECOMMUNICATION: 7 TELECOMUNICATION: 7 
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Patent No. 6303376
GENERAL INFORMATION:
APPLICANT: Glazer, Peter, M.
TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
ADDRESSEE: Patrea L. Pabst
ILON West Peachtree Street
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                                            Indels
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Pred. No. 24;
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                              1 TTGGAGGGGGTGGTGGGG 18
                                                                                                                                                                                            4 TridgAGGGGGriggriggGG 21
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Best Local Similarity 93.33
Matches 14; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-476-712-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-411-291-2
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APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Hogan, Michael E.
APPLICANT: Marumder, Eyves
APPLICANT: Marumder, Eyves
APPLICANT: Marumder, Eyves
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: GO Travis, Suite 1850
CITY: Houston
STATE: Towas
COUNTRY: U.S.A.
ZIP: T7002-2912
COUNTRY: U.S.A.
ZIP: T7002-2912
COMPUTER: BEM PC compatible
OPERATING SYSTEM: MS WAINGOWS 95
SOFTWARE: RIDBY GAS.
SOFTWARE: MS WOR' 97 (Saved as .txt file)
CUASSIFICATION DATA: 435
FILING DATE: 13-OULY-1996
FILING DATE: 13-OULY-95
FILING DATE: 13-OULY-96
APPLICATION NUMBER: GO/01,505
FILING DATE: 19-UULY-96
APPLICATION NUMBER: GO/015,714
FILING DATE: 19-UULY-96
APPLICATION NUMBER: GO/015,714
FILING DATE: 19-WARCH-96
APPLICATION NUMBER: GO/016,714
FILING DATE: 17-ARPIL-96
APPLICATION NUMBER: 1472-06214
FILING DATE: 17-ARPIL-96
APPLICATION NUMBER: 17-ARPIL-96
APPLICATION NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
71.1%; Score 12.8; DB 4;
Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fennewald, Susan
Zendegui, Joseph G.
Ojwang, Joshua O.
Hogan, Michael E.
Pommier, Eyves
Mazumder, Abhijit
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APPLICANT: Rando, Robert F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: DNA (genomic)
US-08-682-255A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGGAGGGGTGGTGGG 17
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-09-429-130-57
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                                                                                                                                                                                                                                                                    US-US-UI-974-57

Sequence 5.7 Application US/99017974

Sequence 5.7 Application US/99017974

Sequence 5.7 Application US/99017974

SEQUENCE INFORMATION:

APPLICANT: Rando, Robert F.

APPLICANT: Hogan, Michael B.

APPLICANT: Gosum, Paul A.

ITILE OF INVENTION: Atti-Viral Guanosine-Rich

TITLE OF INVENTION: Atti-Viral Guanosine-Rich

TITLE OF INVENTION: Atti-Viral Guanosine-Rich

TITLE OF INVENTION: Tetrad Forming Oligonucleotides

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

APPLICANT: Good Travis, Suite 1800

CITY: Houston

STATE: Texas

COMPUTER: TEXAS

COMPUTER: TEXAS

COMPUTER: TEXAS

COMPUTER: TEXAS

COMPUTER: TEXAS

CONFUTER: TEXAS

CONFUTER

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Patent No. 6323185
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennewald, Susan
APPLICANT: Zendegui, Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TGGAGGGGGTGGTGGG 17
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                                                                                                                      1 GGAGGGGGGGGGGG 16
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-682-255A-57
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RESULT 13
US-09-199-542B-19
Sequence 19, Application US/09199542B
Sequence 10, Application US/09199542B
GENERAL INFORMATION:
APPLICANT: Schumm, James W.
APPLICANT: Spreciper, Cynthia J.
TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                               2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Madison:
STATE: Wisconsin
COUNTRY: U.S.A.
2IP: 53711-5399
COMPUTER: U.S.A.
COMPUTER: Diskette - 3.5 inch, 1.44 Mb
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM compatible PC
OPERATING SYSTEM: DOS version 6.0
SOFTWARE: WordPorfect 5.1 (DOS text format)
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/632,575B
FILING DATE: 04/15/96
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE: 09/30/94
INFORMATION FOR SEQ ID NO: 19:
LENGTH: 21
CHARATTERISTICS:
LENGTH: ALICATION NUMBER: DATA:
LENGTH: 21
CHARATTERISTICS:
                                                                                                                                                                                                                Score 12.8; DB 3;
Pred. No. 3.1e+03;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Schumm, James W.
TITLE OF INVENTION: Multiplex Amplification of
TITLE OF INVENTION: Short Tandem Repeat Loci
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Promega Corporation
STREET: 2800 Woods Hollow Road
                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
POTHER INFORMATION: Antisense Oligonucleotide
US-09-490-692-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08632575B Patent No. 5843660
                                                                                                                                                                                                                                                             ,
                                                                                                                                                                                                                Query Match
Rest Local Similarity 87.5%;
Matches 14; Conservative C
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MAP POSITION: D14S562
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    NUMBER OF SEQ ID NOS: 176
SEQ ID NO 35
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-632-575B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-632-575B-19
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Patent No. 6180353
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE: RTS-0120
CURRENT APPLICATION UNMER: US/09/490,692
CURRENT APPLICANTE: 2000-01-24
                                                                                                                                                                                        STATE: TEXAS

COUNTRY: U.S.A.

ZIP: 77002-2912.

ZIP: 77002-2912.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS Windows 95

SOFTWARE: MS Word 97 (saved as .txt file)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/429,130

FILING DATE: 28-Oct-1999

CLASSIFICATION: «UNKNOWN»
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
NUMBER OF SEQUENCES: 87
                                                                         NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33, 962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/682,255
FILING DATE: «Unknown-
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-UULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-WARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-WARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APPLIL-96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MARCH-96
17-APRIL-96
23-APRIL-96
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TELEFAX: 713/238-8008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGGAGGGGGTGGTGGG 17
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-490-692-35
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APPLICANT: Horwitz, Arnold
APPLICANT: Burke, David
APPLICANT: Baltaian, Manik
APPLICANT: Baltaian, Manik
APPLICANT: Baltaian, Mynn S
TITLE OF INVENTION: Stable Bactericidal/Permeability-
TITLE OF INVENTION: Compositions Containing the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: probe upstream of the 1450 point mutation region US-09-809-713-3
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                                                                                                                                                                                                                                                                                                                                                                   Query Match 71.1%; Score 12.8; DB 4; Length 21; Best Local Similarity 87.5%; Pred. No. 3.1e+03; Matches 14; Conservative 0; Mismatches 2; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shuber, Anthony TITLE OF INVENTION: Method For Alteration Detection FILE REFERNCE: EXT-0.47 CURRENT APPLICATION NUMBER: US/09/809,713 CURRENT FILING DATE: 2001-03-15 SOFTWARE: Patentin version 3.0
FILE REFERENCE: 16026/9212

CURRENT APPLICATION NUMBER: US/09/199,542B

CURRENT FILING DATE: 1998-11-25

PRIOR PPLICATION NUMBER: US 08/316,544

PRIOR FILING DATE: 1994-09-30

PRIOR PILING DATE: 1994-09-30

PRIOR FILING DATE: 1966-04-15

NUMBER OF SEQ ID NOS: 110

SOFTWARE: Word97 (CONVERTED to DOS text format)

SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08013801
Patent No. 5420019
GENERAL INFORMATION:
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Patent No. 6428964
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 Tricanciarcacarca 17
                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Homo sapien
LOCATION: D148562
US-09-199-542B-19
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US-08-013-801-4
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US-09-809-713-3
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COUNTRY: 105A

COMPUTER: 105A

COMPUTER: Ploppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25

COMPUTER: Patentin Release #1.0, Version #1.25

CORRENT AFPLICATION NUMBER: 05/08/013,801

FILING DATE: 02 FEB 1993

ATTORNEY/AGENT INFORMATION: 424

ATTORNEY/AGENT INFORMATION: 224

ATTORNEY/AGENT INFORMATION: 21/24/20911

TELEPHONE: 312/346-5750

TELEPHONE: 312/346-5750

TELEPHONE: 312/346-5750

TELEPHONE: 312/346-5750

TELEPHONE: 312/346-5750

TELEPHONE: 312/346-5750

TELEPHONE: 312/346-3740

SEQUENCE CHARACTERISTICS: LENGTH 18;

MOLECULE TYPE: CDNA

UNCECULE TYPE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. ...

E. (bases 1 to 21)

S. Unan, D. Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                  AZ569440 ZM0242012
AZ583408 M0378N23
AZ774703 ZM0004G14
AZ969578 ZM0042G20
AZ307952 IM0010L24
AZ64597 IM0571C07
AZ76951 IM05700018
AZ871408 ZM034E16
BQ901245 HASP002X7
AIZ51781 QH76Q11.X
                                                                                                                                                                                                                                                      AZ62226 IM0455A2

AZ666896 IM0549A24

AZ866896 IM0549A24

AZ866712 IM0564A03

AZ876923 ZM01992D07

AZ876923 ZM01992D07

AZ876324 IM0258F12

AZ876324 IM0258F12

AZ87234 IM0258B07

AZ87234 IM0258B07

AZ87234 IM0258B07

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AZ873198 IM0429D18

AZ8705 IM0522D18

AZ8705 ZM0145M02

AZ8705 ZM0145M02
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AZ381798 1M0138G01
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AI807936 wf52e09.x
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                                    AZ583408
AZ774703
AZ369578
AZ307952
AZ645874
AZ769521
AZ769521
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A5215293
A5666896
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AIS90540
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AZ369361
AZ381798
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AZ405596
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GSS.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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AZ468862
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
AZ468862 IM0282004
AZ760597 IM0584N21
AZ512326 IM0357II8
AZ645269 IM0510810
                                                                                                                                        October 27, 2003, 10:32:29; Search time 1581.77 Seconds (without alignments) 276.576 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                 11152
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                   using sw model
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AZ760597
AZ512326
AZ645269
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gb_gssl:*
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em_estov: *
em_estpl: *
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Match Length
                                                                                                OM nucleic - nucleic search,
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71.1
71.1
71.1
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Post-processing: Minimum DB seq Maximum DB seq

Database

Title: Perfect score:

Run on:

Sequence:

Scoring table:

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Score

No. Result

1113 122.8 122.8

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FEATURES

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F."
/lab host="E. Coli strain XL10-Gold, T1-resistant, F."
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note=="Vector: PWD42IN; Purified genomic DNA from M.
musculus G578L/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ512326
1M0357118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0357118 R, genomic survey sequence.
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Mus musculus
Eukaryota.

Eukaryota.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (Dases 1 to 2)

Dunn,D., Aoyad.A.)

Estam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,A., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse, whole genome scaffolding with paired end reads from 10kb
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University of Utah Genome Center
University of Utah
University of Utah
84112, USA
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                Email: ddunn@genetics.utah.edu
Insert Lengfh: 10000 Std Error: 0.00
Plate: 0554 row: N column: 21
Seg primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
clone="UUGC1M0554N21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ512326.1 GI:10693642
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Unpublished
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AZ512326/c
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ORIGIN
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AUTHORS
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1M0554N21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0554N21 F, genomic survey sequence.
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/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse"
/note="Vector: PWD421vv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
Tel: 801 585 5606
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Pred. No. 5.6e+05;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                     Std Error: 0.00
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Exror: 0
Plate: 0282 row: 0 column: 04
Seq primer: CGTGTAAAAAGGACGGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/arain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0282004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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l Similarity 83.3%; Pro
15; Conservative 0;
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AZ760597/c
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VERSION KEYWORDS

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TITLE

COMMENT

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FEATURES

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untiply //www.jax.orgyresources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWH42 (gi|4732114|gp]_ARI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored for another inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored for ampicallin resistance."
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Innun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Unpublished
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                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0510B10"
                                                                                                                                                                                                                                           High quality sequence stop: 20.
Location/Qualifiers
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Mus musculus
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AZ659755/c
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42IN', Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb zarge using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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Mus musculus
Mus musculus
Busaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalla; Eutheria, Rodentia; Sciurognathi; Muridae, Murinae, Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
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High quality sequence stop: 20.
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AZ645269.1 GI:11774602
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uncoust LVAY mouse LVA RESOURCE (Attrophy) //www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high malar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM42 (qi|4732114|qp|APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampliallin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female" | fab host="B. coli strain XL10-Gold, T1-resistant, F-" | fab host="B. coli strain XL10-Gold, T1-resistant, F-" | foone lib="Mostor: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
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Mus musculus

Bukarica, Rodentia; Craniata; Vertebrata; Euteleostomi;

Bukarica, Metazoa; Chordata; Craniata; Muridae; Murinae; Mus.

I bases I to 21)

I bases I to 21)

I bases I to 21)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, A., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., Mouse whole genome scaffolding with paired end reads from 10kb

Unpublished

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 71.1%; Score 12.8; DB 28; Length 20; Similarity 87.5%; Pred. No. 7.6e+05; 14; Conservative 0; Mismatches 2; Indels (
                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0342 row: O column: 12
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
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Location/Qualifiers
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/clone lib="Mouse lokb plasmid UUGCIM library"
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musculus G57BL/GU (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gp]APL29072 ll), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                            S. 2030 E., SLC,
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                         Biomedical Polymers Research Bldg., 20
                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0537 row: F column: 22
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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AZ969440.1 GI:13840667
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Matches 14; Conservative
                            Rm. 308, Biomedica
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet.
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RESULT 6 AZ969440/c

ò d DEFINITION ACCESSION VERSION

BASE COUNT ORIGIN

KEYWORDS SOURCE ORGANISM

AUTHORS REFERENCE

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musculus C57BL/6/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by sheared DNA
was hydrodynamically sheared by repeated excess. The
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli x110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukarulus
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I (bases I to 21)
Eukarulus, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases I to 21)
Eura, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
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Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                 Rm. 308, Biomedical Polymers Research Bld H12, USS 5606
Fax: 801 585 7177
Email: 6dunn@genetics.utah.edu
Insert Iength: 10000 Std Error: 0.00
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High quality sequence stop: 21.
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Menen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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2M0004G14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004G14 F, genomic survey sequence.
AZ774703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculs G73BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                         Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: N column: 23
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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Mus musculus (house mouse)
Mus musculus
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Matches 14; Conserv
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Laboratory Mouse Down Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agances gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chancally-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mamalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                          Unpublished
Context: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/clone_lib="Mouse_lokb plasmid UDGCIM library"
/note="Wector: PWD421v; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Eaxl: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: L column: 24
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Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
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   plasmid inserts
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AZ645874/c
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                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Tel: 801 585 566
Fax: 801 585 7177
Email: ddunn@genetics utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0242 row: G column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
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1M0010L24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0010L24 F, genomic survey sequence.
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musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 22)
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Mouse whole genome scaffolding with paired end reads from 10kb
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Mus musculus
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/sex="Male" Cols strain XLIO-Gold, T1-resistant, F-" (lab host="E. Cols strain XLIO-Gold, T1-resistant, F-" (lone lib="wouse loke plasmid UUGGIM library" Anone Laborator: PWD42117, Purified genomic DNA from M. musculus CS7BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinaee. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNA42 (gil 4732114) plant29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
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2M0184E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0184E16 F, genomic survey sequence.
         and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., 84112, USA
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                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="museculus"
//organism="museculus"
//do_xergin="G57BL/6J"
//do_xergin="G57BL/6J"
//do_xergin="G57BL/6J"
//do_xergin="G57BL/6J"
//do_xergin="G57BL/GJ"
//do_xergin="Good strain XLI0-Gold, Tl-resistant, F-"
//done lib="Mouse DNb plasmid UUGCIM library"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G77BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
//ttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide Kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size selected for a 9.5 to
10.5 Kb range using preparative agarcse gel
electrophoresis Vector DNA was prepared from a derivative
of PMD42 (g1|4721H|gp]ARL20072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, Ayagai, Ay Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longaoze, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                     S. 2030 E., SLC,
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished
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71.1%; Score 12.8; DB 28; Length 22;
Best Local Similarity 87.5%; Pred. No. 7.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0
                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S.
84112, USA Es 5606
Fax: 801 585 5006
Fax: 801 585 717
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0511 row: C column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 22.
Location/Qualifiers
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Mus musculus
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JOURNAL

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FEATURES

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/organism="Pinus sylvestris/Heterobasidion annosum"
/mol type="mRNR"
/db zref="taxon:169015"
/clone="hasp002xj21f"
/dev stage="Seedling roots of scots pine were infected for dev stage="Seedling roots of scots pine were infected for 6 days with H. annosum"
/clone_lib="Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp)"
/note="Vector: pI-Advy Site_1: BcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (PPS)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 05-NOV-1998
IMAGE:1978032 3'
  Selected Expressed sequence tags of CDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris) Unpublished Contact Fred O. Asiegbu Dept. of Forest Mycology & Pathology Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qu76g01.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032 similar to TR:039949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ;, mRNA
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/lab.host="NGI_CBB"
/clone lib="NCI_CBP Brn35"
/note="Torgan: brain; Vector: pCMV-SPORT6; Site_1: Sall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostoon Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)
NCI/NINDS-Caph http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project Unpublished
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Pred. No. 1.2e+06;
0; Mismatches 3; Indels (
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Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Seg primer: -40UP from Gibco
High quality sequence stop: 1
Location/Qualifiers
                                                                                                                                                                                                            Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbuemykopat.slu.se
Seq primer: T7 primer:
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:1978032"
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82.4%; Prec
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Homo sapiens
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Matches 14; Conserv
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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osum - Scots pine infection stage
Pinus sylvestris/Heterobasidion
        von Niederhausern, A.
                                                                                                                                                                                                                     SLC,
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern, and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC 84112, USA
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hasp002x121f Heterobasidion annosum - Scots pin baspb02x121f Heterobasidion annosum - Scots pin basp0bcraction cDNA library (hasp) Pinus sylvestriannosum cDNA clone hasp002x121f, mRNA sequence:
                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7777
Eax: 801 585 7777
Insert Length: 10000 Std Error: 0.00
Plate: 0184 row: E column: 16
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
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Pinus sylvestris/Heterobasidion annosum
Eukaryota; mixed EST libraries.
1 (bases 1 to 18)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Best Local Similarity 87.5
Matches 14; Conservative
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LOCUS

ACCESSION VERSION KEYWORDS SOURCE

RESULT 14 BQ901245

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ORGANISM

REFERENCE AUTHORS

BASE COUNT ORIGIN

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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade II),
catalog #: 11544-012"

ORIGIN

Query Match

67.8%; Score 12.2; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Search completed: October 27, 2003, 13:59:22 Job time : 1585.77 secs

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October 27, 2003, 10:32:29; Search time 376.114 Seconds (without alignments) 1957.844 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX023402 Sequence	AROZSIZ/ SEQUENCE ARO78333 Seguence	AR173053 Sequence	AX384817 Sequence	AR168831 Sequence	ARZ00300 Sequence AR262431 Seguence	E04543 linker. 9/1	AX659401 Sequence	ARIZ6606 Sequence	A28676 dsRNA with	AR061827 Sequence	AR252818 Sequence	ED16243/ muman art E38866 Chimeric an	E63496 Non-human a	AX488033 Sequence	AZSUSS NUCLEOPIOLE AR221900 Sequence	A02165 Nucleotide	A04686 Nucleotide	ARUZ/664 Sequence	ARI65012 Sequence	AX030648 Sequence	113569 Sequence 13	ISO679 Sequence 13	168183 Sequence 4	187067 Sequence 4	AR036657 Sequence	AR088921 Sequence	ARI52368 Sequence	ARIOSSO4 Sequence AR012712 Sequence	AR036658 Sequence	AR088922 Sequence	AR092032 Sequence	AR149209 Sequence	AX152369 Sequence AX418779 Sequence			linear PAT 15-SEP-2000					WAGNER HERMANN (DE) ;
QI QI	AX023402	4 ~	Š		ლ (⊃ m		AX659401	٥.	A28676	2	AR252818 PR103437	٩		AX488033	AZ5U58 AR221900			o c	AR165012	4	113569 114303	150679	I68183	. :	1 12	2	9	2 =	5	2	ლ ч	2	AR152369 AX418779	ALIGNMENTS		18 bp DNA ent WO0014217.	802			and Wagner, H.	7 16-MAR-2000; ; HEEG KLAUS (DE
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Glazer, P.M.
Methods of targeted mutagenesis using triple-helix forming oligonucleotides
Patent: US 630376-A 2 16-OCT-2001;
Location/Qualifiers
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Pred. No. 3.4e+05;
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Pred, No. 3.3e+05;
0; Mismatches 1;
  74.4%; Score 13.4; DB 6; 93.3%; Pred. No. 3.4e+05; ive 0; Mismatches 1;
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Sequence 17 from Patent WO0210452.
AX384817
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Sequence 2 from patent US 6303376.
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Glazer,P.M.
Triple-helix forming oligonucleotides for targeted mutagenesis
Patent: US 5962426-A 2 05-0CF-1999;
Location/Qualifiers
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G-motif oligonuclectides and uses thereof
Patent: WO 0014217-A 42 16-MAR-2000;
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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         CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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Sequence 42 from Patent WO0014217.
AX023427 GI:10183827
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OS Artificial gene

OC Artificial sequence; Genes.

PD 30-MAR-1993

PP 1993078397-4/18

PD 30-MAR-1991 JP 1991029624

PI YAMAZAN 1291 JP 1991029624

PI YAMAZAN GHIS TAKKSU NAOKO, NEGORO TAKKAATSU, AGUI HIDEO PC

CO7K13/00,A61K37/54,A61K7/54,C12N1/19,C12N1/21,C12N5/10, PC

C12N15/58,C12N15/62,C12N15/70,C12N15/81,C12N15/85//C12P21/02,

PC C12N1/21,C12P21/02,C12R1:19);

CC C12N1/21,C12P21/02,C12R1:19);

CC C12N1/21,L19P1/C12P21/02,C12R1:19);

CC C12N1/21,L19P2/C12R1:19);
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                                                                                                                                                                                                                                                                              PAT 29-SEP-1997
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I chaes 1 to 18)
Yamazaki.C., Takasu,N., Negoro,T. and Agui,H.
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                                                                                               Query Match 71.1%; Score 12.8; DB 6; 18est Local Similarity 87.5%; Pred. No. 6.2e+05; Matches 14; Conservative 0; Mismatches 2;
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/organism="synthetic construct"
/mol type="genomic DNA"
/mol type="taxon:32630"
/db_xref="taxon:32630"
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/organism="unknown"
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1 (bases 1 to 18)

1 (bases 1 to 18)

Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O. and Hogan,M.E. Anti-viral guanosine-rich oligonucleotides and method of treating HIV
                   PAT 17-DEC-2001
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Unclassified.
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I hases I to 18)
Rando, R.F., Fennewald, S., Zendegui, J.G., Ojwang, J.O., Hogan, M.E.,
Pommier, Y. and Mazumder, A.
Guanosine-rich oligomuclectide integrase inhibitors
Patent: US 655785-A 57 12-MAR-2002;
Location/Qualifiers
                                                                                                        Unknown.
Unclassified.
Unclassified.
1 (Jases 1 to 18)
Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
Anti-viral guanosine-rich tetrad forming oligonucleotides
Patent: US 628942-A 57 11-SEP-2001;
Location/Qualifiers
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               AR168831 18 bp 1
Sequence 57 from patent US 6288042.
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AR168831.1 GI:17904956
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Sequence 57 from patent US 6355785.
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AR262431
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
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Sequence 19 from patent US 5843660.
AR061827 GI:5989518
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AR252818
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/organism="unknown"
a 2 c 11 g
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Dean, N.M. and Cowsert, L.M.
Antisense modulation of daxx expression
Patent: US 6180353-A 35 30-JAN-2001;
Location/Qualifiers
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         Patent: WO 02102824-A 3 27-DEC-2002;
Vermicon AG (DE)
Location/Qualifiers
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Sequence 35 from patent US 6180353.
AR126606
AR126606.1 GI:14113199
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87.58;
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Patent: WO 9200375-A
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AR252818.1 GI:27301167

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NCE 1 (bases 1 to 21)

ORS Schumm J.W. and Sprecher.C.J.

ORS Schumm J.W. and Sprecher.C.J.

Los Multiplex amplification of short tandem repeat loci

RNAL Patent: US 6479235.A.19 12-NOV-2002;

Location/Qualifiers

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Search completed: October 27, 2003, 11:09:22 Job time : 380.114 secs

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Reduction, T cell, CD28, gene expression, treatment, immune system disorder, graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, 5'-UTR, systemic lupus erythematosus, inflammatory bowel disease, triplex forming, oligonucleotide, 5'-untranslated region; ss
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95US-0529878.
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AAT36196 standard; DNA; 18
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(first entry)
WO9624380-A1.
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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15-APR-1997
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299.938 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                 hits satisfying chosen parameters:
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Listing first 45 summaries
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AAX90328
AAX90290
AAZ99625
AAZ99650
AAT36197
AAX90329
                                                                                                              nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Gaps

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8 \,
                                                                                                                                                                          Indels
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                                                                                                                                100.0%; Score 18; DB 20;
100.0%; Pred. No. 3.1e+02;
Artive 0; Mismatches 0;
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                                                                                               Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD28 inhibition oligonucleotide RT03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Column 29; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                    Query Match
Best Local Similarity 100...
These 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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                                                            present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USS932556-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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AAZ99625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for inhibiting the expression of CD28, ILL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).

AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, throiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antiganic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
                                                                                                                Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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ses 18; Conservative
  (ICNC ) ICN PHARM INC
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Gaps

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G-motif oligonuclectide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation, natural killer cell; septic shock; cytocoxic T-lymphocyte; inflammation, autoimmune disease; rheumatoid arthritis; Crohn's disease, sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; lyme arthritis; Strepprococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

Nucleotide sequence of non-G-motif oligonucleotide GRF1comp

12-JUL-2000 (first entry)

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The present sequence represents a G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif conjoquicleotides. The G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating released for the ground cells by constituting the uptake of DNA by a cell, by crimulating natural killer cells, or by co-stimulating cytocoxic. Thymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating splic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, and transplant rejection), helper T cell response 1-mediated disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage
                                                                                                                                                                           G-motif oligonucleotide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation; natural killer cell; septic shock; cytocoxic T-lymphocyte; inflammation; autoimmune disease; record arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasati syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomylatis; experimental allergic encephalomylatis; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                                                                             Nucleotide sequence of G-motif oligonucleotide GR1.
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(first entry)
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Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections

Example 14; Page 32; 75pp; English.

(CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH

99WO-EP06502. 98EP-0116652

03-SEP-1999; 03-SEP-1998;

16-MAR-2000

WO200014217-A2

Synthetic.

Heeg K;

Wagner H, Lipford GB, WPI; 2000-256970/22.

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The present sequence represents a non-G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides. The G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells or by co-stimulating cytotoxic. Tlymphocytes The G-motif oligonucleotides may be used for the cross productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, carcoidesis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflections, barasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections), spontaneous and human immunodeficiency virus (HTV)-infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 18; DB 21;
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
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nes 18; Conservative
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ID AAT3
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Gaps

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Length 18; Indels

100.0%; Score 18; DB 21; 100.0%; Pred. No. 3.1e+02;

0; Mismatches

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Local Similarity 100. es 18; Conservative

Best Loca Matches

Query Match

ВР.

AAZ99650/c ID AAZ99650 standard; DNA; 18

AAZ99650

(updated)
(first entry)

25-MAR-2003 15-APR-1997

Synthetic

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Reduction; T cell; CD28; gene expression; treatment; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, throiditis, sarcoides, multiple sclerosis, uveritus, rheumatorid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                        disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                        systemic lupus erythematosus; inflammatory bowel disease;
triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 18; DB 17; Length 2:
100.0%; Pred. No. 3e+02;
....marches 0; Indels
                                                              Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD28 inhibiting phosphorothioate oligonucleotide RT04S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 54; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
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                                                                                                                                                                                                                                                                                                                                 95US-0387041.
95US-0529878.
95US-0387041.
95US-0529878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (ICNC ) ICN PHARM INC
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09-FEB-1995;
18-SEP-1995;
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                                                                                                                                                                                                     Synthetic.
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Gaps

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcuttaneous administration of an oligonucleotide (OGN). AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorochioate oligonucleotide used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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100.0%; Pred. No. 3e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD28 inhibition oligonucleotide RT04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TIGGAGGGGGTGGTGGGG 18
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-443609/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-443609/37.
                                                                                                                                                                                                                                                                                                                                    (TAMR/) TAM R C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAMR/) TAM R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-1995;
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                                                                                          US5932556-A.
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PRANCA STANDARD STAND
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Gaps

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonuclectide (OGN). AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonuclectide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                        CD28; inhibition; antisense oligonuclectide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothicate; ss.
                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                              CD28 inhibiting phosphorothioate oligonucleotide RT09S
                                                                       91.1%; Score 16.4; DB 17; 94.4%; Pred. No. 1.3e+03; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.4; DB 20;
Pred. No. 1.3e+03;
0; Mismatches 1;
in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
                                          Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
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                                                                                                                                   1 TTGGAGGGGGTGGTGGGG 18
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                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                        Conservative
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                                                                                                                                                                                                                                      AAX90336 standard; DNA;
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                                                                                        Local Similarity
ses 17; Conserv
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1995;
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                                                                          Query Match
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Matches
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AAT36242
ID AAT36
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(OGN).
"se in the
                                         The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX80281 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; postrasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; lL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease,
                                                                                                                                                                                                           .
0
                                                                                                                                                                            100.0%; Score 18; DB 20; Length 21; 100.0%; Pred. No. 3e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD28 expression inhibiting oligonucleotide, RT09s.
                                                                                                                                                 Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                                           Pred. No. 3e+
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              Claim 6; Column 29; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                           larity 100.0%;
Conservative 0
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95US-0529878.
95US-0387041.
95US-0529878.
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                                                                                                                                                                                                                                        TTGGAGGGGGTGGTGGGG
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-384228/38.
                                                                                                                                                                                           Local Similarity
les 18; Conserv
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18-SEP-1995;
09-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
16-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                         AAT36243;
                                                                                                                    diseases
                                                                                                                                                                               Query Match
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                                                                                                                                                                                               Best Loca
Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                         disease;
                                                             interleukin 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD28; inhibition, antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
Reduction; T cell; CD28; gene expression; treatment; immune sdisorder; graft versus host disease; septic shock; viral disepsoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleuk; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.8; DB 17;
Pred. No. 5.2e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 45; 77pp; English.
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95US-0529878.
95US-0387041.
95US-0529878.
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                              (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorothioate, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-384228/38.
                                                                                                                                                                                                                                                                                   09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
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                                                                                                                                     Synthetic
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                                                                                                                               Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; sortiasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, e.g. graft versus host disease, septic shock, viral staroiders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic simulation of CD28 positive T cells, with a consequent reduction (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                             CD28 expression inhibiting oligonucleotide, RT05s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD28 expression inhibiting oligonucleotide, RT10s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 45; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                95US-0387041.
95US-0529878.
95US-0387041.
95US-0529878.
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                                                                                                                                                                                                                                                                                                                                                                              96WO-US01507
                                       (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-384228/38.
                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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                                     25-MAR-2003
16-APR-1997
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16-APR-1997
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                                                                                                                                                                                                                                                                 Synthetic
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 AAT36242;
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Matches
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The present invention provides oligonucleotides, and methods for their use, which are useful in modulating the action of proteins involved in gastric acid production. The target protein is preferably the histamine H2 receptor or one of the proteins which form part of the gastric proton pump. The sequences and methods of the invention are useful in the treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers, duodenal ulcers and other gastric acid disturbances, most of which are caused by Helicobacter pylori.
of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonuclectide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the tresent of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonuclectide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by administering an oligonucleotide polypeptide involved in gastric acid
                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gastric acid production inhibiting oligonucleotide SEQ ID NO: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gastric acid disturbance, gastric reflux, gastritis, dyspepsia, stomach ulcer, duodenal ulcer, Helicobacter pylori, antisense,
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                                                                                                                                                                                 Length 18;
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                                                                                                                                                                                                                      Indels
                                                                                                                                                                                 82.2%; Score 14.8; DB 20;
88.9%; Pred. No. 5.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.6%; Score 13.6; DB 22;
81.2%; Pred. No. 1.5e+04;
iive 2; Mismatches 1;
                                                                                                                                                Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 22 BP; 0 A; 0 C; 16 G; 3 T; 3 other;
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 145; 164pp; English
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Matches 13; Conservative
                                                                                                                                                                                                                                                        1 TTGGAGGGGGTGGTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                WPI; 2001-025093/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stomach ulcer; duod
DNA-RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                  AAF16593 standard;
                                                                                                            present invention.
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                                                                                                                                                                                                                                                                                                 The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleocide (OGN). AAX90288 to AAX90281 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorochioate oligonucleotide used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for inhibiting the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
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                                                                                                                                                                                                                    Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8; DB 20;
Pred. No. 5.2e+03;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                          Example; Column 24; 45pp; English
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                                    95US-0529878
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                                                                                                                                                                                 WPI; 1999-443609/37.
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                                                                                                        (TAMR/) TAM R
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                                    18-SEP-1995;
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03-AUG-1999
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em_htg_inv:*
em_htg_other:*
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em_htgo_other:*
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em htg pln: *
em htg rod: *
em htg mam: *
em htg vxt: *
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11. 9p ba:*

31. 9p ba:*

41. 9p ba:*

41. 9p ba:*

41. 9p lintg:*

42. 9p lintg:*

43. 9p lintg:*

44. 9p lintg:*

45. 9p lintg:*

46. 9p lintg:*

47. 9p lintg:*

48. 9p lintg:*

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18
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Maximum DB
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the number of results predicted by chance to have a

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Pred. No.

PAT 29-SEP-1999 AR029999 Sequence
AR103999 Sequence
AR103774 Sequence
BD130004 Asthma-as
BD130004 Asthma-as
BD130004 Asthma-as
AZ7787 Oligonucleo
AX21545 Sequence
AX22501 Sequence
AX029133 Sequence
AR02913 Sequence
AR03952 Sequence
AR03952 Sequence
AR315974 Sequence
AR315974 Sequence
AR315974 Sequence
AR32425 Sequence
AX32425 Sequence
AX32425 Sequence
AX332425 Sequence
AX32425 Sequence
AX32425 Sequence
AX32425 Sequence
AX32425 Sequence
AX32425 Sequence
AX32426 Sequence
AX32436 Sequence
AX314604 Sequence
AX11533 Sequence
AX115459 Sequence
AX215458 Sequence
AX315458 Sequence
AX315458 Sequence
AX315458 Sequence
AX315458 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Unclassified.

1 (bases 1 to 17)
Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 128 19-JAN-1999;
Location/Qualifiers linear DNA 17 bp DN Seguence 128 from patent US 5861244. AR029939 ALIGNMENTS SUMMARIES AR02993 AR02993 AR036446 AR0364467 AR211456 AR211456 AR211456 AR211456 AR211456 AR22201112 AR42220113 AR029133 AR039141 AR212283 AR21283 AR21460 AR21460 AR215469 AR029939.1 GI:5943153 DB Length Query Unknown. Unknown RESULT 1
AR029939/C
LOCUS
DEFINITION
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ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES υo

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                                                                                                                                                                                                                                                                                                    unclassified

unclassified

whison, A. R.B., Buckler, A., Cardon, L., Carey, A.H., Galvin, M., Milson, A. R.B., Buckler, A., Cardon, L., Carey, A.H., Galvin, M., Miller, B., Buckler, A., Cardon, L., Carey, A.H., Galvin, M., Asthma-associated gene

L. Patent: JP 2002500895-A 294
AXYS PHARMACEUTICALS INC
OS Unidentified
AXYS PHARMACEUTICALS INC
OS Unidentified
PP 2002500895-A/294
PP 15-JAN-1998 JP 2000528715
PI ANGENER BROOKS WILSON, ALAN BUCKLER, LON
CARDON, ALISON H CAREY,
PI MARGARET GALVIN, ANDREW MILLER, MICHAEL NORTH
PC C1201/68 A01K67/027, CO7K14/47, C12N15/09, C12N15/00 CC
Strandedness: Single,
CC Asthma-associated gene
FH Key
FT source

//organism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/origanism='/o
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IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED
Location/Qualifiers
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/organism='Unidentified'
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Asthma-associated gene.
BD130004
BD130004.1 GI:23224949
UP 2002500895-A/294.
unidentified
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synthetic construct
artificial sequences.
1 (bases 1 to 22)
Garman,A.J.
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A27787
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BD130004
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Unclassified.
1 (bases 1 to 20)
Miller, A. and North, M.
Asthma related genes
Patent: US 6087485-A 298 11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and Mccarthy, J.J.
Single nucleotide polymorphisms in genes
Parent: WO 0118250-AA 1424 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
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Pred. No. 2.6e+05;
0; Mismatches 1; Indels
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76.7%; Score 13.8; DB 6; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                     Length 17;
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Sequence 298 from patent US 608748S.
AR103774.1 GI:12815362
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Sequence 1424 from Patent WO0118250.
AX096246
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 837 22-NOV-2001,
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Mclaughlin, F.G. Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 818 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) , GLAXO GROUP LIMITED (G
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     Length 17;
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Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
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   71.1%; Score 12.8; DB 6; 87.5%; Pred. No. 4.9e+05; rative 0; Mismatches 2;
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Sequence 837 from Patent WOO188124.
AX422501. GI:21525883
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/crganism="Homo sapiens"
/mol_type="mRNA"
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AX422502.1 GI:21525884
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Query Match
Best Local Similarity 87.5
Matches 14, Conservative
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Method and reagent for the modulation and diagnosis of cd20
mogo gene expression
Patent: WO 0159103-A 899 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd2
mogo gene expression
Patent: WO 0159103-A 898 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Pred. No. 2.6e+05;
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71.1%; Score 12.8; DB 6;
Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2;
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|mol_type="mkNa"
|db_xref="taxon:3263"
|note="Nucleic Acid"
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/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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AX215457.1 GI:15525500
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Sequence 898 from Patent WO0159103.
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AX215456.1 GI:15525499
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Monia,B.P. and Boggs,R.T.
Antisense oligonucleotide modulation of raf gene expression
Patent: US 595229-A 21 14-SEP-1999;
Location/Qualifiers
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87.5%; Pred. No. 4.7e+05;
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S Cook, P. Dan. and Kawasaki, A. Mamoru.

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AL Patent: US 605087-A 9 21-DEC-1999;

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Cook P. Dan. and Kawasaki, A. Mamoru.
2 '-0-modified oligonucleotides
AL Patent: US 5872222-A 9 16-PEB-1999;
Location/Qualifiers
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Sequence 21 from patent US 5952229.
AR073952. GI:10000712
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Sequence 9 from patent US 6005087.
AR096050 GI:10024498
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/organism="unknown"
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Manuyel, P. and Chartier-Harlin, M.
METHOD FOR DIAGNOSING ALZHEIMER DISEASE
METHOD FOR DIAGNOSING ALZHEIMER DISEASE
Betent: WO 9901574-A 2 14-7AN-1999;
INST NAT SANTE RECH MED (FR); AMOUYEL PHILIPPE (FR)
Location/Qualifiers
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1 (bases 1 to 20)
Cook, P.Dan and Kawasaki, A.Mamoru.
2'-modified oligonucleotides
Patent: US 5859221-A 9 12-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                     AR036517 20 bp
Sequence 9 from patent US 5872232.
AR036517
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Seguence 9 from patent US 5859221.
AR029133 GI:5941106
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Sequence 2 from Patent WO9901574
AX001112
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AR036517/c
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(CE 1 (bases 1 to 20)

3RS Love,W.Guy., Nicklin,P.Leslie., Hamilton,K.Ophelia. and Phillips,J.Ann.

JE Liposomal oligonucleotide compositions
ANAL Patent: 105 6096720.A 7 01-AUG-2000,

Location/Qualifiers

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/organism="unknown"

/ Organism="unknown"

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Sequence 7 from patent US 6096720.
AR105507.1 GI:12819104
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1 GGGGAGGAGGGGTGG 16
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Human gene single
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Human c-raf kinase

C-raf kinase

Human FGF receptor

Human ST receptor

Human POSHLI scann

Human POSHLI scann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD28 expression inhibiting oligonucleotide, RT11s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                           ABK00899
ABN07492
ABN07492
ABN07492
ABK18191
AAX18191
AAX18419
AAX185922
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ABK00898
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95US-0529878.
95US-0387041.
95US-0529878.
  96WO-US01507
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(first entry)
 WO9624380-A1
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16-APR-1997
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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 Synthetic
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                                                                                    ; Search time 162 Seconds
(without alignments)
299.938 Million cell updates/sec
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| SIDS1/gcgdata/geneseqn-emb1/NA1980.DAT:*
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score greater than or equal to the score of the result beir
and is derived by analysis of the total score distribution.
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Compugen Ltd.
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            version - 2003 (
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Match Length
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of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for inhibiting the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                        (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, e.g. graft versus host disease, septicularly immune system disease, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uvelits, rheumatorid arthritis, systemic lupus erythematosis, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic simulation of CD28 positive T cells, with a consequent reduction in cycokine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
    treating immune system diseases, e.g. graft vs. host disease,
                                                                                                       present oligonucleotide reduces CD28 dependent interleukin-2
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                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 17;
llarity 100.0%; Pred. No. 3.48+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 1 A; 12 C; 1 G; 4 T; 0 other;
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                                                             Example 2; Page 45; 77pp; English.
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                        septic shock, psoriasis, etc.
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Best Local Similarity
Local 18; Conserve
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                                                                                                                                                                                                                                          The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mallitus, thyroiditis, viral sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lugus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                        ide which reduces CD28 gene expression in T cells immune system diseases, e.g. graft vs. host disease,
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100.0%; Pred. No. 3.4e+02;
ive 0; Mismatches 0;
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(first entry)
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es 18; Conservative
                                                                                                                        Oligo:nucleotide which
(ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ICNC ) ICN PHARM INC
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18-SEP-1995;
09-FEB-1995;
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16-APR-1997
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Matches
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The present sequence represents a polynucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylotycasine for increased triplex stability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex
                                                                                                                                                                                                                                                                                                                                                                                                                              Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) is clinical samples, but also detection of oncogenes and Hepatitis B v
Triple helix third strand of alpha-globin gene nucleotides 827-843.
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                                     DNA detection; triple helix; identification;
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Pred. No. 1.5e+04;
n. Mismatches 2;
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                                                                                                                                                                                                                                                                                                                     (PROF-) PROFILE DIAGNOSTIC SCI INC.
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                                                       bacteria, oncogene, virus; ss
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88.2%;
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92US-0968436.
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Best Local Similarity 86.4
Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-130384/11.
                                     Triplex formation;
                                                                                                               Homo sapiens.
                                                                                                                                                                                                                          22-DEC-1993;
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29-OCT-1992;
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15-FEB-1995
                                                                                           Synthetic.
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                         CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
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               100.0%; Score 18; DB 20; Length 18; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                   CD28 inhibiting phosphorothioate oligonucleotide RT06S.
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100.0%; Pred. No. 3.4e+02;
iive 0; Mismatches 0;
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                                                                                       1 GGGGAGGGGGCTGGAA 18
                                                                                                                             1 GGGGAGGAGGCTGGAA 18
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                                                                                                                                                                                                                        AAX90346 standard; DNA; 18
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                                                                                                                                                                                                                                                                                               (first entry)
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-443609/37
                                   Similarity
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                                                                                                                                                                                                                                                                                               24-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                 Query Match
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                                     Local
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AAX14741/c
                                                                                                                                                                                                        AAX90346/c
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Matches
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Matches
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Gaps

us-09-331-204a-5.szlm22.rng

93WO-US12600. 92US-0999706

28-DEC-1993; 31-DEC-1992;

21-JUL-1994

WO9415945-A1

Synthetic.

Dixon RAF,

Denner LA,

WPI; 1994-249123/30.

Claim 3; Page 9; 53pp;

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The sequence is an antisense molecule directed against position -3 to +18, relative to the start codon of the gene for mouse fibroblast growth factor 1. The polynucleotide can be used for inhibiting vascular smooth muscle cell proliferation and for treating a disease e.g. vascular stenosis, post angioplasty restenosis, athereetomy, atherosclerosis, atrial venous shunt failure, cardiac she also AAQY0313-60. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is an antisense molecule directed against position -6 to +15, relative to the start codon of the gene for mouse fibroblast growth factor 1. The polymuclectide can be used for inhibiting vascular smooth muscle cell proliferation and for treating a disease e.g. vascular stenosis, post angioplasty restenosis, attherectomy, atherosclerosis, atrial venous shunt failure, cardiac
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                                      factor
cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibroblast growth factor, hybridisation, laser procedures, vascular smooth muscle cell; proliferation, SMC; vascular stenosis; post angioplasty restenosis; atherosclerosis; cardiac hypertrophy; organ transplant; ss
                                    growth f
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muscle
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                                    New anti-sense polynucleotide(s) to fibroblast receptor - used for inhibiting vascular smooth proliferation, partic. for treating restenosis
                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense oligonucleotide for mouse FGF.
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AAQ70345 standard; DNA; 21
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(first entry)
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Best Local Similarity 88.4
Best Local Similarity 88.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-249123/30.
WPI; 1994-249123/30
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15-FEB-1995
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(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                    New anti-sense polynucleotide(s) to fibroblast growth factor receptor - used for inhibiting vascular smooth muscle cell proliferation, partic. for treating restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 76.7%; Score 13.8; DB 15; Length 18; Best Local Similarity 88.2%; Pred. No. 1.5e+04; Matches 15; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 3 A; 11 C; 1 G; 3 T; 0 other;
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                                                                                                                                                                                                                            Dixon RA;
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                                                                                                                                                                                                                              Rege AA,
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                                                                                                                                                                                        (TEXA-) TEXAS BIOTECHNOLOGY CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAGGAGGGCTGGAA 18
                                                                                                                                                                                                                                                                                                                                                                                    English
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18 GGGATGTGGGGCTGGAA

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AAQ70342 standard; DNA; 21

AAQ70342/ RESULT

(updated)
(first entry)

25-MAR-2003 15-FEB-1995

AAQ70342;

93WO-US12600 92US-0999706

28-DEC-1993; 31-DEC-1992;

WO9415945-A1 21-JUL-1994

Synthetic

Dixon RAF,

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Denner

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Sequence 21 BP; 2 A; 12 C; 2 G; 5 T; 0 other;
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AAA93151
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AAZ18648
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                                                                                                                                                                                                                                                                                            Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
polymorphism; vascular disease; coronary artery disease; forensics;
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
pulmonary embolism; paternity test; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCarthy JJ;
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids comprising single nucleotide polymorphisms, useful in
                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/standard_name= "single nucleotide polymorphism"
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                                                                    Length 21;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Daley GQ,
  hypertrophy, vascular surgery and organ transplant.
                                                                    DB 15;
                                                                                                                                                                                                                                                                      Human gene single nucleotide polymorphism #1420.
                                                                   76.7%; Score 13.8; DB 15;
88.2%; Pred. No. 1.5e+04;
            See also AAQ70333-60.
(Updated on 25-MAR-2003 to correct PN field.)
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                                               Sequence 21 BP; 4 A; 11 C; 2 G; 4 T; 0 other;
                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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2000US-0220947.
2000US-0225724.
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                                                                                                                                                                                      AAF96659/c
ID AAF96659 standard; DNA; 21
                                                                                                                   2 GGGAGGAGGGGCTGGAA
                                                                                                                                        GGGATGTGGGGCTGGAA
                                                                                                                                                                                                                                                 (first entry)
                                                                               Best Local Similarity 88.2
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-226749/23
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26-JUL-2000;
16-AUG-2000;
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                       Length
                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carey AH;
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Pred. No. 2.1e+04;
0; Mismatches 1;
                       Score 13.8; DB 22;
Pred. No. 1.5e+04;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predisposition to development of asthma
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Galvin M, Miller A, North M;
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                                                                                                                       1 GGGGAGGAGGGCTGGA 17
                       76.7%;
88.2%;
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                                                                           Conservative
                                                                                                                                                                                                                                                                                                 AAZ18648 standard; DNA;
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Query Match
Best Local Similarity
The 15; Conserve
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999.
                                                                                                                                                                                                                                                                                                                                             AAZ18648;
                                                                                                                                                                         21
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GGTGAGGAGGGCTG 19

ASTH1 locus; ASTH11; human; chromosome 11p; asthma; bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predisposition; polymorphism; antibody; drug screening; prophylaxis; therapy; diagnosis; exon boundary; ss.

Homo sapiens

US6087485-A. 11-JUL-2000.

Human ASTH1I gene exon k 5' boundary region.

22-NOV-2000 (first entry)

ВЪ

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New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements -
                                                                  Human secreted protein; cytokine; cell proliferation; nutritional supplement; immune modulation; autoimmune disorder; haematopoiesis regulation; tissue growth; haemostasis; inflammation;
                                                  Clone vq15_1 secreted protein coding sequence probe SEQ ID NO:
                                                                                                                                                                                   99US-0120680.
99US-0198733.
99US-0149639.
99US-0155686.
99US-0157247.
99US-0167822.
                                                                                                                                                                    8-FEB-2000; 2000WO-US04340
AAA93151 standard; DNA; 20
                                  (first entry)
                                                                                                                                                                                                                                                                     (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                     WPI; 2000-549267/50.
                                                                                                                                  WO200049134-A1.
                                                                                                                                                                                                                                                                                      Valenzuela D,
                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                   .5-FEB-2000;
                                                                                                                                                                                              23-APR-1999;
17-AUG-1999;
23-SEP-1999;
                                                                                                                                                                                                                         01-OCT-1999;
29-NOV-1999;
                                 12-JAN-2001
                                                                                                                                                   24-AUG-2000
                                                                                                                                                                                     19-FEB-1999
                                                                                                                                                                                                                                          29-NOV-1999
                                                                                                probe; ss.
                AAA93151;
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New nucleic acids other than naturally occurring chromosomes encoding ASTHI protein, for e.g. screening compositions that modulate expression or function of ASTHI proteins or as diagnostics for genetic predisposition to asthma

Examples; Column 37; 131pp; English.

Rapiejko

Hall J,

Hoffman H,

Yuan O,

Cardon L, Buckler A;

Miller A, North M, son AR, Carey AH;

WPI; 2000-505109/45 Galvin M, Miller Brooks-Wilson AR,

(AXYS-) AXYS PHARM INC.

21-JAN-1997; 01-JUL-1997;

98US-0009913. 97US-0035663.

21-JAN-1998;

The present invention is concerned with a number of secreted proteins and their coding sequences isolated from various human cDNA libraries. The probes shown in the specification (AAA91312-A93186) can be used to obtain the cloned sequences from bacterial cells. The proteins and coding sequences can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic activity, . 0 Score 13.4; DB 21; Length 20; Pred. No. 2.1e+04; 0; Mismatches 1; Indels Seguence 20 BP; 7 A; 1 C; 10 G; 2 T; 0 other; Disclosure; Page 294; 309pp; English ; 0 or anti-inflammatory activity. 74.48; 3 GGAGGAGGGGCTGGA 17 Conservative Query Match Best Local Similarity Matches 14; Conserva' ò

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Gaps
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The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH11 and ASTH11 and ASTH11 genes, which as associated which a genetic predisposition to asthma and common sequence of the ASTH11 and ASTH11 genes are oriented in byposite directions with the ASTH11 and ASTH11 genes are oriented in copposite directions with the ASTH11 and ASTH11 genes are oriented in capression and common sequence motifs. They are both expressed in trachea, lung and several other tissues. ASTH11 and ASTH11 are novel complexed in the activation of a variety of genes including the TCR asthma. Both ASTH11 and ASTH11 mRNAs are alternatively splicing of transcripts has no effect on the open reading crame of ASTH11 and ASTH11 mRNAs are alternatively splicing of transcripts has no effect on the open reading crame of ASTH11 as the exons involved are all 5' to the start codon in the coop in contrast, alternative splicing of ASTH11 transcripts results of the ASTH1 is offerms. The invention also encompasses mouse atthij protein. The ASTH1 nucleic acids are useful as diagnostics to identify a hereditary predisposition to asthma, as probes for identifying atthij proteins, and for generating spression of the gene in a mimals or site specific gene modifications in cell lines The encoded contrast are useful as immunogens to raise specific antibodies; in chargeuring for compositions that mimic or modulate activity or expression of ASTH11 and/or ASTH11 (including altered forms of these corrections, and as a therapeutic. The ASTH1 genes or fragments thereof, and and as a therapeutic. The ASTH1 genes or fragments thereof, corrections that mimic or modulate activity or expression of ASTH11 and/or ASTH11 in the identification of anti-ASTH11 and predise are useful in the identification of individuals are useful in the identification of individuals in vivo for prophylactic and therapeutic purposes. The intaking activity and the are useful in the intended forms and individuals in the intended forms. The prophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in vivo for prophylactic and therapeutic purposes. The intact ASTHII or ASTHIJ proteins or active fragments thereof may be used to modulate or reduce bronchial hyperreactivity. Sequences AAA80550-A80570 represent the exon boundary regions of the human ASTHII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 other;
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Gaps
                                        .
0
    Length 20;
                                           Indels
Query Match
74.4%; Score 13.4; DB 21;
Best Local Similarity 93.3%; Pred. No. 2.1e+04;
Matches 14; Conservative 0; Mismatches 1;
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AAA80555 standard; DNA; 20 BP

RESULT 12 AAA80555

AAA80555

н С

GGAGGAGGGTCTGGA

qq

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BLATT L.
MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                        WPI; 2001-607195/69.
                                                                                                                                                WO200159103-A2.
                                                                                                                       sapiens
                                                                                                                                                                  16-AUG-2001.
                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                       Blatt L,
                                                                                                                      Homo
ö
                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human endothelin converting enzyme-3 protein (ECE-3). ECE-3 is useful for screening selective modulators of vertebrate ECE-3 function, that are useful for treating diseases such as hypertension, arrherosclerosis, vascular restenosis, myocardial ischemia, cerebral vasospasm and subarachnoid hermorrhage, congestive heart failure, diabetes, endotoxic shock, migratine, Raynaud's disease, and also for treating pulmonary disease such as sthma, pulmonary hypertension and adult respiratory distress
                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecule encoding human endothelin converting enzyme-3 protein, useful for screening modulators that are useful for treating atherosclerosis, myocardial and cerebral ischemia, and diabetes
                                                                                                                          ECE-3; endothelin converting enzyme 3; hypertension; artherosclerosis; vascular restenosis; myocardial ischemia; cerebral vascospasm; subarachnoid hermorrhage; congestive heart failure; diabbetes; endotoxic shock; migraine; Raynaud's disease; ss.
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Pred. No. 3e+04;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 3 A; 3 C; 12 G; 3 T; 0 other;
                                                                                                           Primer #2 used to isolate human ECE-3.
                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 40; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%; P. P. les 13; Conservative 0;
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        13
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                                                                                                                                                                                                                                                           99US-0130691.
                                                     AAC68417 standard; DNA; 21
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                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GGÁGGGCTGGAA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GGAGGGCTGGAA 18
        GGTGAGGAGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOGO Inozyme #168.
                                                                                                                                                                                                                                                                                              Bailey WJ,
                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                 WPI; 2000-687323/67.
                                                                                                                                                                                                     WO2.00065025-A2.
                                                                                                                                                                                                                                                          23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-2002
                                                                                         21-FEB-2001
                                                                                                                                                                                                                      02-NOV-2000
                                                                                                                                                                                                                                                                                               Austin CP,
                                                                                                                                                                                   Synthetic
                                                                        AAC68417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   syndrome.
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Matches
                                   RESULT 13
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                                            AAC68417
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Search completed: October 27, 2003, 11:25:19 Job time : 163 secs
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids et a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule motif), a G-Cleaver (cleaving RNA with a NYN motif) pr an amberzyme (cleaving RNA with an NN triplet), a zinzyme (cleaving RNA with an YGY motif). The CD20-targetting nucleic acid is used
                                                                                                                                                                                                                                                                                                                                                       Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; anctoropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; deaver; amberzyme; linzyme; lrymphoma; leukaemia; human; mnunodeflotency virus; HIV associated NHL; lymphom; leukaemia; human immunodeflotency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immuno thrombocycopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer; disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; humanicon's disease; ataxia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury
                                                                                          ..
                                                            Length 17;
                                                       Query Match
71.1%; Score 12.8; DB 23; Length
Best Local Similarity 87.5%; Pred. No. 3.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels
present sequence is an inozyme of the invention.
                            Sequence 17 BP; 0 A; 13 C; 1 G; 3 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chowrira BM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 88; Page 80; 200pp; English
                                                                                                                        1 GGGAGGAGGGCTGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-FEB-2000, 2000US-181797P.
28-FEB-2000, 2000US-185516P.
06-MAR-2000, 2000US-187128P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-FEB-2001; 2001WO-US04273.
                                                                                                                                          17 GGGGAGGAGGGAGG 2
                                                                                                                                                                                                                     )899/c
ABK00899 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                             12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                             Human NOGO Inozyme #169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blatt L, McSwiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLATT L.
MCSWIGGEN J.
CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-607195/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MO200159103-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                               ABK00899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIBO-) (BLAT/) (MCSW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHOM/)
                                                                                                                                                                                                 RESULT 15
ABK00899/c
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QC
2 X 8
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to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the cuse of one or more therapies. In particular, the CD20 targetting CC use of one or more therapies. In particular, the CD20 targetting CC low-grade or follicular non-Hodghin's lymphoma (NHL), bulky lymphoma, low-grade or follicular non-Hodghin's lymphoma (MLL), communocytoma (MC), small B-call lymphocytic leukaemia, HIV (human CC immunocytoma (MC), small B-call lymphocytic lymphoma, immune (MCL), immunocytoma (MC), small B-call lymphocytic lymphoma, immune (MC), immunocytoma elmo, single used to cleave RNA of the NOGO gene in the presence of a clavalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and creatment may further comprise the use of one or more therapies.

CC freat a patient having a condition associated with the level of NOGO. The creatment may further comprise the use of one or more therapies.

CC central nervous system (NS) injury and cerebrovascular accident (CVA, chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), chemotherapy-induced neuropathy, anyotrophic neuropathy accident CVA, chemotherapy-induced neu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Run

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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.

1 (Dases 1 to 22)

1 (Dases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.,

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Fax: 801 585 5006

Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ307952 1000 LORD plasmid UUGCLM library Mus musculus genomic clone UUGCLM0010L24 F, genomic survey sequence.
AZ307952 GI:10347459
A2579495 IM03567C13
A2512534 IM0358B07
A23457234 IM0358B07
A2512326 IM0328A24
A2612326 IM0328A24
A2612326 IM0328A24
A264526 IM0311180
A243710 IM0283118
A243710 IM0295F12
A243710 IM0295F12
A243710 IM0295F12
A2445585 IM0331H02
A253198 IM03295F12
A2657115 IM0295F12
A2657116 IM0296F119
A267714 IM041C07
A266784 IM0429D18 A2671408 A26596 IM0348E16
A29775540 ZM034A216
A2326174 IM048A07
A265975 IM0348E16
A2623037 IM0460X16
A2623037 IM0460X16
A2419284 IM0238E13
A2657189 IM0238E13
A2657189 IM0238E13
A2657141 IM0238E13
A2657141 IM0233E13
A265775 IM040X16
A256775 IM040X16
A256775 IM0338E2
A265775 IM04937E2
A265775 IM04937E2
A265775 IM04937E2
A265776 IM0338E3
A265776 IM0437D13
A261149 IM0437D13
A277511 ZM0307P16
A277511 ZM0307P16
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   AAZS 5 AAZS 6 AA
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    DEFINITION
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
COMMENT
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AZ307952
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AA968729 Or69h11.s
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                             22781392 segs, 12152238056 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                         nucleic search, using sw model
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18
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2:: em_estbum:.*
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6:: em_estbum:.*
10:: em_estbum:.*
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10:: em_estbur:.*
11:: gb_htc:.*
13:: gb_est2:.*
13:: gb_est4:.*
13:: gb_est4:.*
13:: em_est6...
13:: em_est6...
14:: em_gss_hum:.*
15: em_gss_hum:.*
16:: em_gss_hum:.*
19:: em_gss_hum:.*
22:: em_gss_hum:.*
23:: em_gss_hum:.*
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27:: em_gss_hum:.*
28:: em_gss_hum:.*
29:: em_gss_hum:.*
29:: em_gss_hum:.*
20:: em_gss_hum:.*
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Match Length
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11.8
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Perfect score:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Kato,K. and Maroba,R.
Generation of expressed sequence tags from mouse brain
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
Nara Institute of Science and Technology
18916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5581
Email: kkatoobs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12; DB 9; Length 16; Pred. No. 1.1e+06;
found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                Trace considered overall poor quality Insert Length: 514 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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/db_xref="taxon:10090"
/clone="BED0002246"
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TITLE
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COMMENT
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AU254493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Labusatory whose DNA wesource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb]AP129072.13, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored for another chemically competent E. coli xiio-Gold (Stratagene) cells and selected for amplcillin resistance."
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Email: cgapbs-r@mail.nih.gov

Email: block, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genere Clone distribution: Old-CGAP clone distribution can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 27-AUG-1998
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or69h11.s1 NCI_CGAP_GC3 Homo 8apiens cDNA clone IMAGE:1601157 3'
similar to SW:PRPE_HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
/lab hos=="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab hos=="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksor
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       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                       Insert Length: 10000 Std Error:
Plate: 0010 row: L column: 24
Seq primer: CGTTGTAAAAGGAGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0010L24"
                                                                                                                                                                       High quality sequence stop: 22.
Location/Qualifiers
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TITLE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (qi|4792114|jub|APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0358B07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0358B07 F, genomic survey sequence.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
2 (bases 1 to 20)
2 (bases 2 to 20)
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86.7%; Pred. No. 1.3e+06;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: C column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0367C13"
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Location/Qualifiers
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Matches 13; Conserv
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AZ512534.1
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84112, US
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AZ512534/c
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                                                                                                                                                                                                                                        19 bp mRNA linear EST 17-DEC-1999 wc74e09.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2324392 3' similar to TR:Q01942 Q01942 EXTENSIN ;contains element TAR1 A1696833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancras; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DAS Sequencing By: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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1M0367C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0367C13 F, genomic survey sequence.
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1 (bases 1 to 19)

Nati-CGAP http://www.nobi.nlm.nih.gov/noicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP); Tumor Gene Index
Unpublished
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.3e+06;
); Mismatches 2; Indels
                   Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGB:2324392"
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AZ579495.1 GI:11693924
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86.7%;
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Homo sapiens
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                                                                           1 GGGGAGGAGGGG
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REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

FEATURES

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at conseant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWM42 (qi|4772114) qpl/APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically completent E. coli XL10.Gold (Stratagene) cells and 1 c. 17 g
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                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 19).

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb
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/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Insert Length: 10000 C dd Brror: 0.00
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
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Fax: 801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by respected by
no binch orifice at constant velocity. The sheared DNA
was blunt enda-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|A1229072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L. (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0358 row: B column: 07
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/63"
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/clone="UUGC1M0358B07"
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Location/Qualifiers
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Gaps

ACCESSION VERSION KEYWORDS SOURCE

RESULT 7 AZ345792 H

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified genomic_DNA_from M.
musculus_C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse_DNA_Resources/Accuments/Anares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch oritice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by repeated by
norliceotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-0old (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                          Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
10 (bases 1 to 20)
11 (bases 1 to 20)
12 (bases 1 to 20)
13 (bases 1 to 20)
14 (bases 1 to 20)
15 (bases 1 to 20)
16 (bases 1 to 20)
17 (bases 1 to 20)
18 (bases 1 t
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81.2%; Pred. No. 2e+06;
tive 0; Mismatches 3; Indels
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84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
seq primer: CACACAGGAAACAGCTATGACC
class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
mol_type="genomic DNA"
strain="CS7BL/61"
/db xref="taxon:10090"
/clone="UUGCIM0357118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                               Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                       AUTHORS
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               KEYWORDS
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AZ512326 GI:10693642
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Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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/clone lib="Mouse 10%b plasmid UUGCIM library"
/note="Wetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plates 10328 row: A column: 24
Seq prime: CGTGTAAAACGACGGCCAGT
class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 19.
Location/Qualifiers
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Best Local Similarity
Matches 13; Conserv
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84112, US
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AZ512326/c
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AUTHORS
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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

JOURNAL

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TITLE

FEATURES

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/clone libs "Mouse lott plasmid UDGIM library"
//clone libs "Mouse lott plasmid UDGIM library"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was Mydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor of ligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                               Mus musculus (house mouse)
Mus musculus
Bukaziota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaziota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 20)
Dunn,D., Aoyagi, S., Mabrer,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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Insert Length: 10000 Std Error: 0.00
Plate: 0563 row: L column: 18
Seg primer: CACACAGGAAACAGCTAATGACC
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/organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
                             AZ772707.1 GI:12896303
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13; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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Best Local S:
Matches 13
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                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Duval, B., Mannole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Job host="E. Coli strain XLIO-Gold, TI-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
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Class: plasmid ends
High quality sequence stop: 20.
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                                                           Mus musculus (house mouse)
Mus musculus
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AZ969440 200 DNA linear GSS 27-APR-2001 2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

AZ772707 100583L18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0583L18 R, genomic survey sequence.

RESULT 11 AZ772707/c LOCUS DEFINITION

BASE COUNT ORIGIN

Matches

ò a

Gaps

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Inductory Wouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with 74 DNA polymerase and 74
polymuclectide kinase. Adaptor oligoniclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 gb| APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
IMO219P12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIMO219P12 R, genomic survey sequence.
AZA33710
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Uppublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
"m 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse lokb plasmid UGGIM library" /note="Vector: PWD42nv, Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jacksor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0219 row: P column: 12
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Location/Qualifiers
                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
                                                                                                      AZ433710.1 GI:10557723
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AZ476392/c
                                                                                                                                                                                     ORGANISM
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AUTHORS
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                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 20)
Dunn, D., Aoyag, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., Von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                   clone UUGC2M0242012 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                       Mus musculus (house mouse)
Mus musculus
                                                AZ969440.1 GI:13840667
GSS.
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AUTHORS
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COMMENT
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                                                                      VERSION
KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil [473214][6]] API29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Fr. 108, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                        AZ495585
1M0331H02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0331H02 R, genomic survey sequence.
                                                                                                                                                                                                      Mus musculus (house mouse)

Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa; Chordata; Coiurognathi; Muridae; Murinae; Mus.

(bases 1 to 21)

Eum, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mainmoud, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
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81.2%; Pred. No. 2e+06;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A4112, USA
Tel: 801 585 5606
Fax: 801 585 717
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0331 row: H column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0331H02"
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13; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of DWD42 (4)4792114 [gb/H229072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
... 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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0
                       GSS 04-OCT-2000
                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
Bunn, D., Aoyagia, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
1 bp DNA linear GSS 04-OCT-200 1M0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0295F12 F, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0295F12"
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Location/Qualifiers
                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
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21 GGGGTGGGGGGGGGGG

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20 GGGGGGGAGGGGGGG 5

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Search completed: October 27, 2003, 13:59:24 Job time: 1583.77 secs

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Sequence 127, App
Sequence 128, App
Sequence 128, App
Sequence 128, App
Sequence 2, Appli
                                                                                                                                                                                                           12, Appl
17, Appl
68, Appli
6, Appli
57, Appli
68, Appli
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from alpha-1-
DESCRIPTION: globin sequence region in Seq ID No. 5861244127
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US-08-579-223-15
PCT-US94-13-15
US-08-12847A-15
US-08-128-128
US-09-225-2018-128
US-09-225-2018-128
US-08-57-210A-2
PCT-US93-12600-17
US-08-483-122-5
US-08-483-122-5
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COMPUTER READABLE FORM:
MEDIUM TYREA
COMPUTER: 18M PC/XT/AT
SOFTWARE: Wordperfect Version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US 07/966,436
FILING DATE: 29 OCT 1992
ATTONNEY/AGENT INFORMATION:
NAME: Handelman, JOSEPH H.
REGISTRATION NUMBER: 26,179
REGISTRATION NUMBER: 26,179
REGISTRATION NUMBER: 26,179
TELEPHONE: (ALLCATION)
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EDNESS: single stranded
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PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID
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         Sequence 128, App
Sequence 11, Appl
Sequence 10, Appl
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Sequence 13, A
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                   GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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PCTT-US93-12600-11
PCT-US93-12600-11
US-08-12600-13
US-08-126-13
US-08-126-13
US-08-126-13
US-08-126-13
US-08-136-136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                       - nucleic search, using sw model
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18
1 9999a99a999ct99aa 18
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Gapop 10.0 , Gapext 1.0
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length: 22
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Perfect score:
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Sequence 13, Application PC/TUS9312600
GENERAL INFORMATION:
APPLICANT: Denner, Larry A.
APPLICANT: Denner, Larry A.
APPLICANT: Dason, Richard A.F.
TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A
FINEDESSEE: Desealer, Goldsmith, Shore &
ADDRESSEE: Desealer, Goldsmith, Shore &
ADDRESSEE: Milnamow, Led,
STREET: 180 North Stetson, Suite 4700
CITTY: Chicago
STREET: 111inois
COUNTRY: USA
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                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk Compatible Computible Computible Computible Compatible Compatible Compatible Computible Compatible Corputible Seffware: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12600
FILING DATE: 28-DEC-1993
CLASSTRICATION:
PRICE 28-DEC-1993
CLASSTRICATION:
PRICE DECEMBER: US 07/999,706
FILING DATE: DECEMBER: US 07/999,706
FILING DATE: DECEMBER: US 07/999,706
FILING DATE: DECEMBER: US 07/999,706
FILING NUMBER: S. DECEMBER: S. DECEMBER: S. DECEMBER TINCRMATION:
NAME: KRIZ, MATTIN L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
PPLICATION NUMBER: PCT/US93/12600
FILING DATE: 28-DEC-1993
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGAGGAGGGCTGGAA 18
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.2'
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                     ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
NUMBER OF SEQUENCES:
                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US93-12600-13/c
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APPLICANT: Rege, Ajay A.
APPLICANT: Rege, Ajay A.
APPLICANT: Dixon, Richard A.F.
TITLE OF INVENTION: ANTISBNSE MOLECULES DIRECTED AGAINST A
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY
                                                                                                                                                                                                                                                    RESULT 2
PCT-US33-12600-11/c
PCT-US33-12600-11/c
Sequence 11, Application PC/TUS9312600
GENERAL INFORMATION:
APPLICANT: Rege, Ajay A.
APPLICANT: Dixon, Richard A.F.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY NUMBER OF SEQUENCES: PERSONDENCE ADDRESS:
ADDRESSE: Minamow, Ltd.
ADDRESSEE: Minamow, Ltd.
STREET: 180 North Stetson, Suite 4700
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88.2%; Pred. No. 1.4e+03;
Live 0; Mismatches 2; Indels
                        Length 17;
                     Ouery Match
76.7%; Score 13.8; DB 2; Length 1
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US93/12600
FILING DATE: 28-DEC-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dressler, Goldsmith, Shore & ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: 111inois
COUNTRY: USA
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APPLICATION NUMBER: US 07/999,706
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US93-12600-10/c; Sequence 10, Application PC/TUS9312600; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGAGGGGCTGGAA 18
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MOLECULE TYPE: DNA (genomic)
                                                                                                                              1 GGGGAGGAGGGCTGGA 17
                                                                                                                                                                               17 GGGGAGGAGGGAAGGA 1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
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WESOUT'S

Sequence 21, Application US/08250856A

Patent No. 585355

BAPPLICANT: Monia, Brett P. and Boggs, Russell T.

TITLE OF INVENTION: Antisense Oligonucleotide Modulation
CORPERSE LAW Offices of Jame Massey Licata
STATE: No 8002

COMPUTER READABLE FORM:
MEDIUM TIPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM S6/2

COMPUTER: IBM S6/2

COMPUTER: MAY 31, 1994

CLASSIFICATION NUMBER: US/08/250,856A

FILING DATE: MAY 31, 1994

CLASSIFICATION NUMBER: 15PH-0094

FILING DATE: MAY 31, 1994

CLASSIFICATION NUMBER: 32,257

REPREMEDED DOCKET NUMBER: 32,257

REPREMEDED DOCKET NUMBER: 33,257

REPREMEDED DOCKET NUMBER: 33,2940

TELEPHAN: (609) 779-2400

TELEPHAN: (609) 779-2400

TELEPHAN: (609) 779-2400

SEQUENCE CHARACTERISTICS: LANGTH. CARRETT LANGTH. CARRETTERS

FANGTH. CARRETTERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGAGGAGGGGTGG 16
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: Sing
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-250-856A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.7%; Score 13.8; DB 5; Length 21;
88.2%; Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: 285 Hamilton Ave, Suite 200
CITY: 0430
COUNTRY: USA
ZIPE: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: 1 EBM Compatible
COMPUTER: 1 EBM COMPAT:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-49
TELECOMMUNICATION INFRMATION:
TELECHOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 298, Application US/09009913; Sequence 298, Application US/09009913; Patent No. 6087485; GENERAL INFORMATION:
APPLICATION NUMBER: US 07/999, FILING DATE: December 31, 1995
ATTORNEY/AGENT INFORMATION:
NAME: KALE, MAITH L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-540
INFORMATION FOR SEC 125,1616-5460
INFORMATION FOR 
             US 07/999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGAGGAGGGCTGGAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                        linear
E: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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MOLECULE TYPE:
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US-09-009-913-298
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US-08-756-806A-21/C
Sequence 21, Application US/08756806A
Fatent No. 595229
Fatent No. 595229
FATELE OF INVENTION: Antisense Oligonucleotide Modulation
TITLE OF INVENTION: of raf Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o;
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: 1EM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                         Query Match
71.1%; Score 12.8; DB 2;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2;
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Pred. No. 3.7e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURPOILER: 15M '50'
COPERATING SYSTEM: PC-DOS
SOTTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,806A
FILING DATE: No. 595229ember 26, 1996
CLASSIFICATION S.56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07111
FILING DATE: May 31, 1995
FILING DATE: May 31, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licate
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0200
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.1%;
87.5%;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.5:
Matches 14; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTL-SENSE: yes
US-08-471-973A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acid
EDNESS: Single
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TI-SENSE: Yes
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                                   SEQUENCE CHARACT
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Sequence 9, Application US/08471973A
Sequence 9. Application US/08471973A
Sequence 9. Application US/08471973A
Septent No. 5872232
APPLICANT: Phillip Dan Cook
APPLICANT: Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 587223Zris
STREET: One Liberty Place - 46th Floor
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: 18M PC compatible
COMPUTER: 18M PC computer: 18M PC compatible
COMPUTER: 18M PC computer: 18M PC comp
                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMRUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WardPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,037A
FILING DATE: 06-JUN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 835,932
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INPORMATION:
NUMBER: JOSEPH LUCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISIS-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 1GIS.
TELECHMUNICATION INFORMATION:
TELEPHONE: 215-566-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33,307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 ddddaddaddadcodd 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...AGTERISTIC
20 bases
2 res. nucleic acid
STRANDEDNESS: single
7 DOPOLOGY: linear
7 ANTI-SBNE: yes
US-08-468-037A-9
Query M-7
Ba-7
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Best Local Similarity
Matches 14; Conserva
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RESULT 12
US-09-143-21/C
US-09-143-21/C
Sequence 21, Application US/09143214
Fatent Wo. 609066
Fatent Wo. 609066
Fatent Workwarion:
CENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Of raf Gene Expression
FITLE OF SEQUENCES: 65
CORRESPONDENCES: 65
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 66 East Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MAILON
STATE: MAILON
STATE: MAILON
COUNTRY: USA
ZIDURYPE: USA
ZIDURYPER EADABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPRFEET 5.1
CURRING APPLICATION DATA:
APPLICATION NUMBER: US/09/143,214
FILING DATE:
CLASSIFICATION NUMBER: US/09/143,214
APPLICATION NUMBER: PCT/US95,806
FILING DATE: NO. 6090626ember 26, 1996
FILING DATE: MAY 31, 1995
FILING DATE: MAY 31, 1995
FILING DATE: MAY 31, 1995
FILING DATE: MAY 31, 1994
APPLICATION NUMBER: 08/250,856
FILING DATE: MAY 31, 1994
ATTORNEY AGENT INFORMATION:
NAME: Jane MASSEY Licata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
71.1%; Score 12.8; DB 3;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                      ISIS-2004
                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,357
FLING DATE:
PLING SPETCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,037
                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32,257
                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 20 bases TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION
TELEPHONE: (609) 779-2400
TELEFAX: (609) 810-1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGAGGAGGGGCTGG 16
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 GGGGAGGAGGGGG
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ANTI-SENSE: yes
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                                                                                     Sequence 9, Application US/08465880

Patent No. 595589
GENERAL INFORMATION:
APPLICANT: Philip Dan Cook
TITLE OF INVENTION: Gapped 2' Modified Oligonucleotides
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5955589ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6005087ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Patent No. 6005087
GENERAL INFORMATION:
GAPPLICANT: Phillip Dan Cook
APPLICANT: A. Kawasaki
TITLE OF INVENTION: 2'-Modified Oligonucleotides
CORRESPONDENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              CITY:

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MDIUM TYPE: 3. inch disk, 720 Kb

COMPUTER: BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordberfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,880

CLASSIFICATION DATA:
APPLICATION NUMBER: 244,993
FILING DATE: 2.1-JUN-1994

ATTORNEY/ACENT INFORMATION:
MAME: Joseph Lucci
REGISTRATION NUMBER: 131.00

REFERENCE/DOCKET NUMBER: 131.00

TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMA
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERSTICS:
1.FNGTH: 20 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 GGGGAGGAGGAGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-035-357-9/c
                                                                 JS-08-465-880-9/c
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) Sequence 21, Application US/09506073
) Patent No. 6410518
) GENERAL INFORMATION:
) APPLICANT: Monia, Brett P.
) TITLE OF INVENTION:
) FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.8; DB 4;
Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.8; DB 4;
Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE KEFERNOTE OF THE CONTREMENT OF THE KEFERNOTE COURRENT FILING DATE: 2000-02-18
CURRENT FILING DATE: 2000-02-18
EARLIER APPLICATION NUMBER: US 09/143,214
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-0-06
EARLIER FILING DATE: 1999-0-06
EARLIER PILING DATE: 1999-0-06
EARLIER APPLICATION NUMBER: US 08/756,806
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1996-11-26
EARLIER FILING DATE: 1996-11-26
EARLIER FILING DATE: 1996-11-26
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1994-05-31
NUMBER OF SEQ 1D NOS: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.1%; Score 12.8; Eilarity 87.5%; Pred. No. 3.7e Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         ISIS-2005
                  COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 KD
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: antisense sequence US-09-506-073-21
                                                                                                                                                                                            US/09/135,202
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,973
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: JOSEPH LUCCI
REGISTRATION NUMBER: 33.307
REFERENCE/DOCKET NUMBER: ISIS-200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGAGGAGGGCTGG 16
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87.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: SIT

TOPOLOGY: linear

ANTI-SENSE: yes

US-09-135-202-9
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Best Local Similarity
                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
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US-09-506-073-21/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: alternative oligonucleotide with uniform OTHER INFORMATION: phosphorothiate backbone with nucleotides 10-20 OCHER INFORMATION: being substituted by methoxy at the 2' position of OTHER INFORMATION: the sugar moiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09135202
Patent No. 6399754
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cock
APPLICANT: Andrew Kawaski
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCE: 37
CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz and No. 6399754ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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Patent No. 6095720
GENERAL INFORMATION:
APPLICANT: Sharman, Thomas
APPLICANT: Abrarman, Thomas
APPLICANT: Phillips, Judith A
APPLICANT: Phillips, Judith A
APPLICANT: Hamilton, Karen O
TITLE OF INVENTION: Liposomal Oligonuclectide Compositions
FILE REPERENCE: 4-20536/A/MA 212
CURRENT FILING DATE: 1999-04-23
GURRENT FILING DATE: 1999-04-23
FARLIER PPLICATION NUMBER: GB 9515743.4
FARLIER PLING DATE: 1995-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.1%; Score 12.8; DB 3; Length 20; 87.5%; Pred. No. 3.7e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                               Length 20;
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                                                                                                                                                                                          Score 12.8; DB 3;
Pred. No. 3.7e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: phosphorothicate backbone FEATURE:
                                                                                                                                                                                          Query Match
Best Local Similarity 87.5%; Pr
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                               1 GGGGAGGAGGGCTGG 16
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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Matches 14; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                              Nucleic Acid
EDNESS: Single
                                                                                STRANDEDNESS: Sir
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-09-143-214-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-135-202-9/c
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US-09-000-136-7/c
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                    SEQUENCE C
LENGTH:
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Conservative	
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Search completed: October 27, 2003, 14:03:34 Job time: 42.3143 secs

Sequence Sequence

Sequence 901, App Sequence 1935, App Sequence 122, Appli Sequence 14, Appli Sequence 11, Appli Sequence 11, Appli Sequence 8086, App Sequence 8086, App Sequence 140, App Sequence 140, App Sequence 15, App Sequence 16, Appli Sequence 16, Appli Sequence 6, Appli Sequence 16, Appli

US-09-780-533A-46
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US-09-780-533A-901
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US-09-108-10-1035
US-10-108-10-1035
US-10-108-10-1035
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US-09-9730-617-16
US-09-9730-617-16
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Sequence

ALIGNMENTS

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US-09-666-108-7464

US-09-666-108-7464

US-09-666-108-7464

Sequence 7464, Application US/09866108

Patent No. US20020049800A1

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: FRANK, David R.

APPLICANT: RANK, David R.

APPLICANT: SIANNON, MASER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR FILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR PLILING DATE: 2001-01-30

PRIOR PRIUR DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PRIUR DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PRIUR DATE: 2001-01-30

PRIOR PRIU
  Sequence 7484, Ap Sequence 7485, Ap Sequence 898, App Sequence 899, App Sequence 9, App11 Sequence 21, App11 Sequence 7486, Ap Sequence 7486, App Sequence 7486, App Sequence 7486, App Sequence 7486, App Sequence 7486, Ap
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                                                                                                                        October 27, 2003, 11:25:34; Search time 387.943 Seconds (without alignments) 124.432 Million cell updates/sec
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2: /cgn2_6/prodata/1/pubpna/USO7 PUBCOMB.seq:*

3: /cgn2_6/prodata/1/pubpna/USO6 PUBCOMB.seq:*

3: /cgn2_6/prodata/1/pubpna/USO6 PUBCOMB.seq:*

4: /cgn2_6/prodata/1/pubpna/USO6 PUBCOMB.seq:*

5: /cgn2_6/prodata/1/pubpna/PCTUG9 PUBCOMB.seq:*

6: /cgn2_6/prodata/1/pubpna/PCTUG9 PUBCOMB.seq:*

7: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

8: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

11: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

13: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

14: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

15: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

16: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

17: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

16: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

17: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

18: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*

17: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-96-26-9
US-09-866-108-7486
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                                                                                                                                                                                                                                                                                                                                      1792395 seqs, 1340900451 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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length: 22
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Perfect score:
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Maximum DB seq
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Sequence 899, Application US/09780533A

| Publication No. US20030060611A1
| GENERAL INFORMATION | US20030060611A1
| GENERAL INFORMATION | US20030060611A1
| APPLICANT | Ribazywe Pharmaceuticals, Inc. | |
| APPLICANT | Blatt, Larry |
| APPLICANT | Blatt, Larry |
| APPLICANT | Blatt | Dete |
| TITLE OF INVENTION | Method and Reagent for the Inhibition of NOGO Gene |
| TITLE OF INVENTION | Method 978-A (400/011) |
| CURRENT PILING DATE: 2001-02-09 |
| PRIOR APPLICATION NUMBER: US 60/181,797 |
| PRIOR APPLICATION NUMBER: US 60/181,797 |
| NUMBER OF SEQ ID NOS: 6679 |
| SEQ ID NO 899 |
| SEQ ID NO 890 |
| SEQ ID NO 890 |
| SEQ ID NO 890 |
| SEQ ID NO 800 |
| S
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                                                                                                                                                                                                                                                                                                Gaps
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71.1%; Score 12.8; DB 11; Length 17;
Best Local Similarity. 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels (
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                                                                                                                                                                                                             Length 17;
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                                                                                                                                                                                                    71.1%; Score 12.8; DB 9; ilarity 87.5%; Pred. No. 2.5e+04; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
8-09-780-533A-898/c
; Sequence 898, Application US/09780533A
; Publication No. US20030060611A1
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87.5%;
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CRGANISM: Homo sapiens
US-09-780-533A-898
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ORGANISM: Homo sapiens
        LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Mensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ABONICAT: US/09/866,108
CURRENT APPLICATION NUMBER: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 2.5e+04;
0; Mismatches 2; Indels
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PRIOR DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-05-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
SCOTTWARE: Acomica Sequence Listing Engine
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7485, Application US/09866108
Patent No. US20220048800A1
APPLICANT: GU, Yizhong
APPLICANT: GI, Yozhong
APPLICANT: PENN, Sharron G, APPLICANT: PENN, Sharron G, APPLICANT: HANZEL, David K.
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87.5%;
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Best Local Similarity 87.5
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108-7484
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US-10-057-550-21/C

Sequence 21, Application US/10057550

Publication No. US2003032607A1

GENERAL INFORMATION:

APPLICANT: Monia, Brett P.

ITLE REPERENCE:

CURRENT APPLICATION NUMBER: US/10/057,550

CURRENT APPLICATION NUMBER: US/56,073

PRIOR FILING DATE: 2000-02-18

PRIOR PLING DATE: 1998-08-28

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1998-09-06

PRIOR FILING DATE: 1998-07-06

PRIOR FILING DATE: 1996-01-26

PRIOR FILING DATE: 1996-01-26

PRIOR FILING DATE: 1996-01-26

PRIOR FILING DATE: 1996-01-26
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Publication No. US20030187240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cook, Phillip Dan
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: 2' Modified Oligonucleotides
FILE REFERENCE: ISISS137
CURRENT APPLICATION NUMBER: US/10/352,586
CURRENT APPLICATION NUMBER: 09/389,283
PRIOR PILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                            71.1%; Score 12.8; DB 11;
llarity 87.5%; Pred. No. 2.4e+04;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.1%; Score 12.8; DB 12; Best Local Similarity 87.5%; Pred. No. 2.4e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                    ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Synthetic construct US-10-352-586-9
                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             1 GGGGAGGAGGGCCTGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Matches 14; Conserv
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Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325Alris
STREET: One Liberty Place - 46th Floor
  Gaps
  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 71.1%; Score 12.8; DB 12; Length 17; Best Local Similarity 97.5%; Pred. No. 2.55+04; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                Sequence 45, Application US/10133779
Publication No. US20030165884A1
GENERAL INDORMATION:
APPLICANT: Chow, Robert
APPLICANT: Tonai, Richard
APPLICANT: Tonai, Richard
TILE REFERENCE: 020035-000210US
CURRENT APPLICATION High Throughput Methods of HLA Typing
FILE REFERENCE: 020035-000210US
CURRENT APPLICATION NUMBER: US/10/133,779
CURRENT FILING DATE: 2002-075
PRIOR APPLICATION NUMBER: US/09/747,391
PRIOR PILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 278
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 45
LENGTH: 17
  Indels
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MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,263
FILING DATE: 28-No. US20030004325A1-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/471,973
PRIOR APPLICATION NUMBER: 08/471,973
ATTORNEY/AGENT INFORMATION:
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REGIGSTRATION UNMBERR: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2005
TELECOMMUNICATION INFORMATION:
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08996263
Publication No. US20030004325A1
GENERAL INFORMATION:
0
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                                             1 GGGGAGGAGGGCTGG 16
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                                                                             GGGGAGGAGGGGAGG 1
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ZIP: 19103
COMPUTER READABLE FORM:
  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                             RESULT 5
US-10-133-779-45
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Matches
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APPLICANT: GHEN, MACHINE GENE EXPRESSED IN HUMAN HEART AND MUSCLE TILLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE TILLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-27

PRIOR FILING DATE: 2000-05-27

PRIOR FILING DATE: 2000-05-27

PRIOR FILING DATE: 2000-05-27

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00666

PRIOR APPLICATION NUMBER: PCT/USO1/00669

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PRIING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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APPLICANT: GU, Yizhong
APPLICANT: Fenn, Sharron G.
APPLICANT: Fordgang
APPLICANT: Fordgang
APPLICANT: ANNX David R.
APPLICANT: CHEN, Wenshang
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
FRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-36
PRIOR APPLICATION NUMBER: GB 24263.6
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68.9%; Score 12.4; DB 9;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1;
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Patent No. US20020048800A1
GENERAL INFORMATION:
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US-09-866-108-7486
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71.1%; Score 12.8; DB 14; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels (
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71.1%; Score 12.8; DB 14;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2;
PRIOR APPLICATION NUMBER: PCT/US95/07111
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/250,856
PRIOR FILING DATE: 1994-05-31
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 21
LENGTH: 20
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, OTHER INFORMATION: antisense sequence US-10-173-2258-21
                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: antisense sequence US-10-057-550-21
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US-09-866-108-7486
Sequence 7486, Application US/09866108
Patent No. US200204880A1
GENERAL INFORMATION:
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                                                                                                                                                                                          TYPE: DNA
ORGANISM: artificial sequence
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APPLICANT: U, Yonggang
PPLICANT: PENN, Sharron G
APPLICANT: HANZEL, David K.
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Pred. No. 3.7e+04;
0; Mismatches 1;
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Publication No. US20030166229A1
GENERAL INPORMATION:
APPLICANT: Shannon, Mark
ITILE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: P80178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
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TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
                                                     NUMBER OF SEQ ID NOS; 4162
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1931
LENGTH: 17
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Publication No. US20030166229A1
GENERAL INFORMATION:
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Best Local Similarity 92.9%;
Matches 13; Conservative
                              PRIOR FILING DATE: 2001-10-10
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Best Local Similarity 92.9
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-10-061-201-1931
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; ORGANISM: Homo sapiens
US-10-061-201-1932
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US-10-061-201-1932/c
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TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN I
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN I
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN I
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT PILING DATE: 2002-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLLING DATE: 2000-02-7
PRIOR PLLING DATE: 2000-02-7
PRIOR PLLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2001-01-30
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SEQ ID NO 7487
LENGTH: 17
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Publication No. US20030166229A1
GENERAL INFORMATION:
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92.9%;
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Best Local Similarity 92.97
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-7487
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; TYPE: DNA

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PUBLICATION NO. US2003016622941
GENERAL INFORMATION:
APPLICAMY: Shannon, Mark
TITLE OF INVENTION: HUWAN POSH-LIKE PROTEIN 1
FILE REPERENCE: P80178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
1 GGGGAGGAGGGCT 14
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Best Local Similarity
Matches 13; Conserv
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US-10-061-201-1934/c
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| ORGANISM: Homo sapiens | US-10-061-201-1934 | G8.9%; Score 12.4; DB 12; Length 17; Query Match | Samilarity | 92.9%; Pred. No. 3.7e+04; Matches | 13; Conservative | O; Mismatches | 1; Indels | O; Gaps | Organization | Organizatio
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                                                                                                                                                                               October 27, 2003, 10:32:35; Search time 2356.29 Seconds (without alignments) 253.343 Million cell updates/sec
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| CGD2_6|ptodata/1|pna/USG0_COMB.seq:*
| CGD2_6|ptodata/1|pna/USG0_BCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/pna/US099F
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Perfect score:
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Sequence 2, Appli
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| pna/US6019_COMB.seq:+
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| pna/US6021_COMB.seq:+
| pna/US6022_COMB.seq:+
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US-09-331-204A-5
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US-10-310-188-60578
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US-T0*303~1/8-3363	US-10-310-188-5892	US-10-227-565-61140	US-10-310-188-84932	US-10-367-832A-61140 US-10-310-188-24767	US-10-310-188-61077	US-10-310-188-61084 US-10-310-188-41819	US-10-310-188-41829	US-10-310-188-41830	US-10-303-778-1410 US-10-310-188-42169	US-10-310-188-18119	US-IU-303-778-I678U 113-08-170-096-11	US-10-266-090-38012	PCT-US03-07273-12	PCT-USU3-07273-165 PCT-11803-07273-12	PCT-US03-07273-165	US-08-170-096-10	US-US-1/U-UVB-L3 TS-09-657-472-1424	US-10-310-188-39028	US-10-310-188-18209	US-10-303-778-14517 US-10-303-778-1396	US-10-310-188-84403	US-10-310-188-5724	PCT-US00-04340-82 PCT-IIS98-01260-298	FCT-US00-04340-82	PCT-US98-01260-298	US-09-507-209-82 US-09-511-446-298	US-10-266-090-45537	US-10-303-778-5139	US-10-310-188-18091	ALIGNMENTS	1204 IGO APTAMERS SPONSE 709/331,204 20 7US97/23927 0 f Artific of ribonucl s term inclusterm inclusterm inclusterm	10. 00 00.
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Score 18; DB 19; Length 18; Pred. No. 3.2e+03;

100.0%;

Query Match Best Local Similarity

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DEFICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INNENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Response of Modulating an Immune Response of Interest also of 18/09/331, 204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 20
LENGTH: 18
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US-10-188-60578

Sequence 60579, Application US/10310188

GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
TITLE OF INVENTION: USES THEREOF
FILE REPERRENCE: 47487
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100.0%; Score 18; DB 19;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 0;
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Mismatches
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US-09-131-204A-20/c
Sequence 20, Application US/09331204A
GENERAL INFORMATION:
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ORGANISM: synthetic construct
US-09-331-204A-20
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, ORGANISM: synthetic construct
US-09-331-204A-5
18; Conservative
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LENGTH: 18
Matches
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; LOCATION: (5963161)...(5963177)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6548
US-10-227-565-61140
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CTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6548
PCT-US02-25943-61140
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TITLE OF INVENTION: BIOIRFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 84932
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                                     CENTERAL INFORMATION:
Sequence 61140, Application PC/TUS0225943
GENERAL INFORMATION:
SEQUENCE 61140, Application PC/TUS0225943
GENERAL INFORMATION:
PRICE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SSG ID NO 61140
LENGTH: 17
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANTON: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Peeudomonas aeruginosa PA01, complete genome;
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PADLICATION NUMBER: US/10/227,565
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 61140
LENGTH: 17
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 8.9e+04;
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US-10-310-188-84932
; Sequence 84932, Application US/10310188
; GENERAL INFORMATION:
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Best Local Similarity 93.8%; Pr
Matches 15; Conservative 0;
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Matches 15, Conservative
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US-10-227-565-61140/c
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
FILLE OP INVENTION: USES THEREOF
FILLE REPERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
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GENERAL INFORMATION:
APPLICANT: ROSCETEGENOMICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
SEQ ID NO 3565
LENGTH: 16
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Pred. No. 8.9e+04;
0; Mismatches 1; Indels 0
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Pred. No. 8.9e+04;
0; Mismatches 1;
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Pred. No. 3.6e+04;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 66578
LENGTH: 22
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Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-310-188-60578
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US-10-303-778-3565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-310-188-5892
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Best Local Similarity
'-hes 15, Conserv
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US-10-303-778-3565/c
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US-10-310-188-5892/c
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LENGTH: 16
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Sequence 41819, Application US/10310188

Sequence 41819, Sequence 61819, Seque
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GER TITLE OF INVENTION: USES THEREOF FILE REFREENCE: 4748 CURRENT APPLICATION NUMBER: US/10/310,188 CURRENT APPLICATION NUMBER: US/10/310,188 CURRENT FILING DATE: 2002-12-19 NUMBER OF SEQ ID NOS: 86641 SOFTWARE: Patentin version 3.1 SEQ ID NO 61077 LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61084, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSELTAGEmonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN-
TITLE OF INVENTION: USES THEREOF
FILE PERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEC ID NOS: 86841
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.4; DB 50;
Pred. No. 8.9e+04;
0; Mismatches 1;
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Pred. No. 8.9e+04;
0; Mismatches 1;
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-61084
                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo sapiens US-10-310-188-61077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-310-188-41819
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LENGTH: 18
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Sequence 24767, Application US/10310188

GENERAL INFORMATION:
APPLICANT: RosettaGemonics
APPLICANT: RosettaGemonics
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION UNMBER: US/10/310,188
CURRENT PAPLICATION UNMBER: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Parentin version 3.1
SEQ ID NO 24767
LENGTH: 18
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 65484
US-10-367-832A-61140
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TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REPERBINGE. Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SEG ID NO 61140
LENGTH: 17
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80.0%; Score 14.4; DB 50; Length 17;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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US-10-367-832A-61140/c
; Sequence 61140, Application US/10367832A
; GENERAL INPORMATION:
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US-10-188-61077
Sequence 61077, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSettaGemonics
                                                                                                                                                                                                                                                         1 GGGGAGGAGGGCTGG 16
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Best Local Similarity 93.8
Matches 15; Conservative
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US-10-310-188-24767
                  ; ORGANISM: Homo sapiens
US-10-310-188-84932
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US-10-310-188-24767
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Sequence 60578, Application PC/TUS0238216
| Sequence 60578, Application PC/TUS0238216
| GENERAL INFORMATION:
| APPLICANT: ROSSIC Genomics LTD
| TITLE OF INVENTION: GENES AND USES THEREOF
| FILLE REPERENCE: 55002
| CURRENT APPLICATION NUMBER: PCT/US02/38216
| CURRENT FILING DATE: 2002-11-12
| NUMBER OF SEQ ID NOS: 86641
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 60578
| LENGTH: 22
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Sequence 5892, Application PC/TUS0238216
Sequence 5892, Application PC/TUS0238216
Sequence 5892, Application PC/TUS0238216
GENERAL INFORMATION:
GENERAL TO SECUENCE OF INVENTION:
TITLE OF INVENTION:
GENES AND USES THEREOF
TITLE OF INVENTION:
GENES AND USES THEREOF
TITLE OF SEQUENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 5892
LENGTH: 16
   Sequence 48851
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PCT-USO2-38216-10450
PCT-USC2-38216-10450
PCT-USC2-38216-1034
US-10-271-602B-105
PCT-USC2-38216-6031
PCT-USC2-38216-6030
PCT-USC2-38216-6455
PCT-USC2-38216-6445
PCT-USC2-38216-6445
PCT-USC2-38216-39006
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PCT-USC2-38216-60897
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93.8%; Pred. No. 1.1e+04;
ive 0; Mismatches 1;
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Best Local Similarity 93.8
Matches 15, Conservative
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         TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-60578
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Matches 16; Conserv
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; TYPE: DNA
; ORGANISM: HOMO 80
PCT-USO2-38216-5892
             Query Match
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2: /cgn2 6/ptcdata/1/pna/USO6_NEW_COMB.seq:*

3: /cgn2 6/ptcdata/1/pna/USO7_NEW_COMB.seq:*

4: /cgn2 6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

5: /cgn2 6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

6: /cgn2 6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

7: /cgn2 6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

7: /cgn2 6/ptcdata/1/pna/USO8_NEW_COMB.seq:*
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Compugen Ltd.
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PCT-US02-38216-60794
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                                    GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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seq length: 22
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Score

Result õ Post-processing:

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Minimum DB Maximum DB

Title: Perfect score:

Sequence:

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Sequence 41819, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
NUMBER OF SEQ ID NOS: 86841
SOCTWARE: Patentin version 3.2
SEQ ID NO 41819
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                           PCT-US02-38216-61084

SEQUENCE 61084, Application PC/TUS0238216

SEQUENCE 61084, Application PC/TUS0238216

GENERAL INFORMATION:

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REPERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT APPLICATION NUMBER: PCT/US02/38216

SUGNEMAR OF SEQ ID NOS: 86841

SOFTWARE PARENTH Version 3.2

SEQ ID NO 61084
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GENERAL INPORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
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                                                                                           80.0%; Score 14.4; DB 1;
93.8%; Pred. No. 1.1e+04;
iive 0; Mismatches 1;
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80.0%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1;
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                                                                                             Query Match
Best Local Similarity 93.8
Matches 15, Conservative
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Best Local Similarity 93.8
Matches 15, Conservative
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; ORGANISM: Homo sapiens
pCT-USO2-38216-41819
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, ORGANISM: Homo sapiens
PCT-US02-38216-61084
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-61077
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PCT-US02-38216-41829
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Sequence 61077, Application PC/TUS0238216
GENERAL INFORMATION.
APPLICANT ROSELTA Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION UNMARER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE PARENTH PLANCE DATE: 2002-11-12
SEQ ID NO 61077
LENGTH: 18
                                                                                                                                                Sequence 84932, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: ROSECTA Genomics LTD
TITLE OF INVENTION: GENES AND USES THEREOF
FILE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: PATENTIN VERSION 3.2
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
FITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VEYSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 1.1e+04;
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  GGAGGAGGGCTGGAA 18
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                                                16 GGAGGAGGGGCTGGCA 1
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Hes. 15, Conservative
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, ORGANISM: Homo sapiens
PCT-US02-38216-24767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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LENGTH: 18
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Best Loca Matches

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GENES AND USES THEREOF

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SECT-US02-38216-18209
| Sequence 18209, Application PC/TUS0238216
| GENERAL INFORMATION:
| APPLICANT: Rosetta Genomics LTD
| TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
| TITLE OF INVENTION: GENES AND USES THEREOF
| FILLE PEPERENCE: 55002
| CURRENT APPLICATION NUMBER: PCT/US02/38216
| COFFRENT APPLICATION NUMBER: PCT/US02/38216
| COFFRENT APPLICATION NUMBER: PCT/US02/38216
                                                                                              Sequence 1819, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BOING SEATHEREOF
TITLE OF ENVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION UNMER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 18119
LENGTH: 20
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76.7%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39026, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: ROSELTA GENOMICS LID
TITLE OF INVENTION: BIOINFORMATICALLY DETECTAR:
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VETSION 3,2
SEQ ID NO 39028
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Best Local Similarity 100.0
Matches 14; Conservative
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CRGANISM: Homo sapiens
PCT-US02-38216-18209
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANISM: Homo sapiens
PCT-US02-38216-18119
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PCT-US02-38216-39028
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Sequence 41830, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT FILING NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFFWARE: Patentin version 3.2
LENGTH: 21
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| Sequence 42169, Application PC/TUS0238216
| GENERAL INFORMATION
| APPLICANT: ROSetta Genomics LTD
| ITLLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
| TITLE OF INVENTION: GENES AND USES THEREOF
| CURRENT PAPLICANTION NUMBER: PCT/US02/38216
| CURRENT FILING DATE: 2002-11-12
| NUMBER OF SEQ ID NOS: 86841
| SEQ ID NO 42169
| LENGTH: 22
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Pred. No. 1e+04;
0; Mismatches 1; Indels
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFREENCE: 55002
CURRENT APPLICATION NUMBER: PCT/USO2/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 41829
LENGTH: 21
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
PCT-US02-38216-41829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Homo sapiens
PCT-US02-38216-41830
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PCT-US02-38216-42169
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Sequence 5724, Application PC/TUS0238216
Sequence 5724, Application PC/TUS0238216
GENERAL IMPORMATION:
APPLICANT: ROSELTA Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFRENCE: 55002
CURRENT APPLICALTON NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SEQ TRANS PARENTIN VERSION 3.2
SEQ ID NO 5724
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROSELTA Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT PELLIG DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 84403
LENGTH: 18
TYPE: DAA
ORGANISM: Homo sapiens
PCT-US02-38216-84403
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Query Match 76.7%; Score 13.8; DB 1; Length 22; Best Local Similarity 88.2%; Pred. No. 1.8e+04; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                               RESULT 14
PCT-1902-38216-84403/c
; Sequence 84403, Application PC/TUS0238216
; GENERAL INFORMATION:
                                                                                                             1 GGGGAGGAGGGCTGGA 17
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PCT-US02-38216-5724
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Search completed: October 27, 2003, 18:22:55 Job time : 307.029 secs

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October 27, 2003, 10:32:29 ; Search time 438.8 Seconds (without alignments) 1957.844 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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PAT 19-MAR-2002
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Glazer, P.M.
Methods of targeted mutagenesis using triple-helix forming oligonucleotides
Patent: US 630376-A 2 16-OCT-2001;
Location/Qualifiers
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Matches 16; Conservative 0; Mismatches 3; Indels
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Sequence 2 from patent US 6303376.
AR173053.1 GI:17912544
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Sequence 17 from Patent WO0210452.
AX384817
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Best Local Similarity 84.2
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Unclassified.
1 (bases 1 to 20)
Glazer,P.M.
Triple-helix forming oligonucleotides for targeted mutagenesis Patent: US 5962426-A 2 05-0CT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    Lipford,G.B., Heeg,K. and Wagner,H.
G-motif Oligonucleotides and uses thereof
Patent: WO 0014217-A 42 16-WAR-2000,
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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//organism="synthetic construct"
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Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 18; Conservative 0; Mismatches 0;
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Sequence 2 from patent US 5962426.
AR078333.1 GI:10005079
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Sequence 42 from Patent W00014217.
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Unclassified.
1 (bases 1 to 20)
Ballinger, D.G., Ding, W., Wagner, S. and Hess, M.A.
Chromosome 11-linked coronary heart disease susceptibility gene CHD1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.

1 (bases 1 to 20)
Acton, S.Laurene.
Intronic and polymorphic SR-BI nucleic acids and uses therefor Patent: US 5998141-A 56 07-DEC-1999;
Location/Qualifiers
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Acton, S. Laurene.
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Pred. No. 4e+05;
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                                                                                 Patent: US 6225451-A 204 01-MAY-2001;
Location/Qualifiers
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Location/Qualifiers
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Sequence 56 from patent US 5998141.
AR092032.1 GI:10018786
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Method and nucleic acids for the analysis of colon cancer
Patent: WO 03014388-A 245 20-FEB-2003;
Epigenomics AG (DE)
Location/Qualifiers
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/note="Detection oligonucleotide for pl6"
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/note="Detection oligonucleotide for pl6"
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Sequence 204 from patent US 6225451.
AR148843
                18 bp D1
Sequence 243 from Patent WO03014388.
AX705574.1 GI:29562239
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Sequence 245 from Patent W003014388.
AX705576.1 GI:29562241
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Unclassified.
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Matson.R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 12 09-Nov-1999;
Location/Qualifiers
                                                    Unclassified.

I (bases 1 to 21)
Masson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 11 09-NOV-1999;
Location/Qualifiers
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1 (bases 1 to 21)

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Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas. Oligomucleotide repeat arrays
Patent: US 5981185-A 48 09-NOV-1999;
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AR084559
AR084559.1 GI:10011330
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Sequence 12 from patent US 5981185.
AR084523.1 GI:10011294
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Matches 16; Conservative 0
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Unclassified.
Unclassified.
(Dasse 1 to 20)
Acton, S.L. and Ordovas, J.M.
Human intronic and polymorphic SR-BI nucleic acids and uses therefor
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Cohen.D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
patent: US 6537751-A 9409 25-MAR-2003;
Location/Qualifiers
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Pred. No. 5.8e+05;
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Location/Qualifiers
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Sequence 56 from patent US 6228581.
AR149209.1 GI:15113800
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11 c 0 g
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Location/Qualifiers /organism="unknown"

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BASE COUNT ORIGIN

PAT 01-SEP-2000

linear

DNA

21 bp | Sequence 11 from patent US 5981185. ARO84522

LOCUS DEFINITION ACCESSION

RESULT 13 AR084522/c

0; Gaps Query Match 61.9%; Score 13; DB 6; Length 21; Best Local Similarity 76.2%; Pred. No. 6.9e+05; Matches 16; Conservative 0; Mismatches 5; Indels ò

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Search completed: October 27, 2003, 11:09:25 Job time: 439.8 secs

21 GTGGTGGTGGTGGTGGTG 1

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0 0 0 0 0
                           ; Search time 189 Seconds
(without alignments)
299.938 Million cell updates/sec
   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                          2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
                    - nucleic search, using sw model
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AAX90336 AAT36242 AAX30335 AAX90335 AAX90337 AAX90034 AAT40012 AAT40012 AAT40012 AAT40012 AAT40012 AAT40012 AAT40012 AAT40013

ALIGNMENTS

RESULT 1

N Geneseq 19Jun03:*

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Human tissue kalli CD28 expression in Viral integrase in Oligonuclectide #4 CD28 inhibiting ph

AAŽ99630 ABK99296 ABK99296 AAC61998 AAC61997 AAC97897 AAC97897 AAC97897 AAC9364 AAC9364 AAT3645 AAT3645 AAT3645

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Database

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Reduction, T cell, CD28, gene expression, treatment, immune system, disorder, graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, 5'-UTR, systemic lupus erythematosus, inflammatory bowel disease, triplex forming, oligonucleotide, 5'-untranslated region, ss
                                                                                                                                                                                                                                                                                                                                                                       Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
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18-SEP-1995;
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15-APR-1997
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AAT36197

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Triplex forming ol CD28 inhibiting ph CD28 inhibiting ph Triplex forming ol CD28 inhibiting ph CD28 inhibition ol Nucleotide sequenc Nucleotide sequenc

AAT36197 AAX90329 AAX90291 AAT36196 AAX90328 AAX90290 AAZ99620

220010 220010

221 221 221 18 18 18 18

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Description

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Query Match

Score

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD28, inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
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100.0%; Pred. No. 56;
cive 0; Mismatches 0;
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Pred. No. 56;
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                                                                                             Seguence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD28 inhibition oligonucleotide RT04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Column 29; 45pp; English.
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                                                         present invention
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                                                                                                                              Query Match
Best Local S
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AAT36196
ID AAT3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                         The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft varsus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, throiditis, sarcoides, multiple sclerosis, uverlits, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                              Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGTTGGAGGGGGTGGTGGGG 21
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     (ICNC ) ICN PHARM INC
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                                                                             WPI; 1996-384228/38
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                                           Tam RC;
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25-MAR-2003 15-APR-1997

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Synthetic.

15-AUG-1996

09-FEB-1995;

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Tam RC;

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expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
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                                                                                                                                                                                                                                                                                                     Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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Pred. No. 7e+02;
0; Mismatches 0; Indels
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100.08; Fr.
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hes 18; Conservative
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AAX90290
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                                                                                                  Reduction, T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; arcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonuclectide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, e.g. graft versus host disease, septic shock, viral disease, partiasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                   Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
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Pred. No.
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100.0%; Pre
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95US-0529878.
95US-0387041.
95US-0529878.
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               (updated)
(first entry)
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Best Local Similarity
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09-FEB-1995;
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AAX90328;

RESULT

AAX90328
ID AAX9
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DT 24-S
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CD28
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KW immv
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Matches

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Gaps

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Gaps ö

Score 18; DB 20; Length 18; Pred. No. 7e+02; 0; Mismatches 0; Indels

Bb

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN) . AAX90288 to AAX90281 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-motif oligonucleotide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation, natural Killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease, rheumatoid arthritis; crohi sdisease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis, streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomycablits; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid architis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of G-motif oligonucleotide GR1.
                                                                                                                                                                                     Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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                  Claim 5; Column 29; 45pp; English
                                                                                                                                                                                                                          / Match 85.7%; SC Local Similarity 100.0%; P
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                                                                                                                                                                                                                                                                                                       4 TIGGAGGGGTGGTGGGG 21
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                                                                                                                                                    diseases.
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                                                                                                                                                                                                                                                                     Matches
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98EP-0116652 99WO-EP06502

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disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allargic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, paraštic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV) infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage precursor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection; antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allargic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; parasitic infection; Lumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a non-G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthitis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence of non-G-motif oligonucleotide GRF1comp
                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                             Score 18; DB 21; Length 16
Pred. No. 7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                            Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                       Local Similarity 100.
Les 18; Conservative
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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleoride (OGN).

AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
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                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD28 inhibiting phosphorothioate oligonucleotide RT09S.
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                                                                                                         17;
                                                                                                         Score 16.4; DB 17;
Pred. No. 2.7e+03;
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      in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
                                                                  Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
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Best Local Similarity 94.4%;
Marches 17; Conservative
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 94.4'
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AAX90336
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disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced archritis, Lyme archritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelltis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV) -infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reduction, T cell, CD28, gene expression, treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; postriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uvetis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligo:nucleotide which reduces CD28 gene expression in T cells -
for treating immune system diseases, e.g. graft vs. host disease,
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O
                                                                                                                                                                                                                                                     Score 18; DB 21; Length 18;
Pred. No. 7e+02;
0: Mismatches 0; Indels
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                                                                                                                                                                                                                   Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
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100.0%; Pre
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95US-0529878.
95US-0387041.
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(first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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18-SEP-1995;
09-FEB-1995;
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16-APR-1997
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Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematoous; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, e.g. graft versus host disease, septicularly immune system disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveritis, theumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic simulation of CD28 positive T cells, with a consequent reduction (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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Pred. No. 1e+04;
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18-SEP-1995;
09-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, vuveitis, theumatical artifitis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytckine release.
                                                                                                                                Reduction, T cell, CD28, gene expression, treatment, immune system disorder, graft versus host disease; septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides; multiple sclerosis, uveitis, rheumatoid arthritis, interleukin 2, systemic lupus erythematosus; inflammatory bowel disease; IL-2; production, antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease,
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                                                                                                    CD28 expression inhibiting oligonucleotide, RT05s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.8; DB 17;
Pred. No. 1e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
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95US-0529878.
95US-0387041.
95US-0529878.
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16; Conserv
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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16-APR-1997
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Gaps

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Query Match Best Local S:

Matches

AAT36244;

XEXELXEX

AAT36244

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CD28

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of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutagen incorporated for site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            supF gene, triplex forming mutagenic oligonucleotide; pso-AGT20;
4'hydroxymethyl-4,5',8-trimethylpsoralenated; site specific; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           supF gene triplex forming mutagenic oligonucleotide pso-AGT20.
                                                                                                                                                                            Length 18;
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Pred. No. 1.7e+04;
0; Mismatches 3;
                                                                                                                                                                        / Match 10.5%; Score 14.8; DB 20; Local Similarity 88.9%; Pred. No. 1e+04; es 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "4'hydroxymethyl-4,5',
B-trimethylpsoralenated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mutagenic oligo:nucleotide(s) - having a m
in an oligo:nucleotide which forms a triplex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 field.)
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                                                                                                                                           Seguence 18 BP, 1 A, 2 C, 11 G, 4 T, 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific mutation. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 38; 72pp; English
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                           present invention
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modified_base
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22-SEP-1995
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Matches
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                                                                                                                                                                                                                                                                                               The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorchioate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes a method for inhibiting the expression
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                                                                                                                                                                                                                 Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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70.5%; Score 14.8; DB 20;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.
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                                        18-SEP-1995;
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AAX90337
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Search completed: October 27, 2003, 11:25:19 Job time : 189 secs

AZ969440 2M0242012 AZ476392 1M0295F12

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Was musculus (house mouse)

Mus musculus

Musculus

Musculus

Musculus

Musculus

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musculus

1 (bases 1 to 22)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacze,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished

Contact: Robert B. Weiss

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

RA112. USA

Tel: 801 585 5606

Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZE45874 1005 IND Linear GSS 14-DEC-2000 LMO511C07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0511C07 R, genomic survey sequence.
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                                      BC585098
AZ331098
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AZ86882
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RESULT 1
AZ645874/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
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COMMENT
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AZ766712 1M0564A03
AZ871408 2M0184E16
AZ666896 1M0549A24
                                                                                             Search time 1845.4 Seconds (without alignments) 276.576 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Compugen Ltd.
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Copyright (c) 1993 - 2003
                                                                     using sw model
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unacounty incluse but accounted for the bunk was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared bus of the orifice at constant velocity. The sheared bus was blunt end-repaired with T4 bus polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 5. to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwh94 (qi|4732114|qp|APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptores complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.Gold (Stratagene) cells and selected for amplial in resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0564 row: A column: 03

Seq primer: CACACAGGAAACAGTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers
                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0564A03"
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1M0564A03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic

clone UUGCIM0564A03 R, genomic survey sequence.

AZ766712. GI:12884063
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Waiss, R., Stokes, R., Tingey, A., von Niederhausern, A., Mouse whole genome scaffolding with paired end reads from 10kb
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University of Utah Genome Center
University of Utah
Rm. 389, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
Tel: 801 585 5606
                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XLIO-Gold, Ti-resistant, F-"/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6U (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0511C07"
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 108, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UTGCIM library"
/note="Vector: PWD42Irv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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69.5%; Score 14.6; DB 28; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 4; Indels (
Tel: 801 585 5606
Pax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0184 row: E column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="CS7BL/6J"
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'clone="UUGC2M0184E16"
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Location/Qualifiers
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AZ666896.1 GI:11804042
                                                                                                                                                                                                                                                                                                                                                                       sex="Male"
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AZ666896/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel. electrophoresis. Vector DNA was prepared from a derivative of pmp42 (gil 47321141gbl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0242012 F, genomic survey sequence.
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 20)
Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UGCOM library"
/note="Vector: PWD47ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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80.0%; Pred. No. 6.2e+05;
tive 0; Mismatches 4;
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0549 row: A column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
High quality sequence stop: 20.

One of the column 
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="UUGC1M0549A24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGTTGGAGGGGGTGGTGGGG 21
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FEATURES

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/Bab.maie".
/Jab hoss="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note=="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gfrom a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XILO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
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80.0%; Pred. No. 6.2e+05;
live 0; Mismatches 4; Indels (
                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 12
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/6J"
                                                                                                                                                                                                                                                                                                       High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0295F12"
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AA911600.1 GI:3050964
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male'
               University of Utah
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TITLE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female" coli strain XLIO-Gold, TI-resistant, F-"
/lab host="E. coli strain XLIO-Gold, TI-resistant, F-"
/clone lib="Mouse DIXb plastified genomic DNA from M.
/note="Wedcuts DNA Resource from the Jackson Laboratory Mouse DNA Resource from the Jackson Laboratory Mouse DNA Resource from the Jackson (http://www.jax.org/resources/documents/dnares/). The DNA was bydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 k brange using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pMA42 (4)147221072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored for and stransformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for amplilin resistance."
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Dunn, Aoyadia, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                     S. 2030 E., SLC,
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Pred. No. 6.2e+05;
0; Mismatches 4; Indels
                  Biomedical Polymers Research Bldg., 20
                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Fax: 802 585 7177
Fax: 804 585 7177
Fate: 0.242 row: 0 column: 12
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol type="genomic DNA"
ferrain="C57BL/60"
/db xref="taxon:1009"
/clone="UUGC2M0242012"
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University of Utah Genome Center
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AZ476392.1 GI:10634517
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1 Similarity 80.0%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
308, E. USA
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RESULT 6 AZ476392/c

g ò

LOCUS

BASE COUNT ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

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Gaps

us-09-331-204a-6.szlm22.rst

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/sex="Male"
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Best Local Similarity
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AZ331988
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KEYWORDS
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E 1 (bases 1 to 22)
S Herwig,R., Schulz,B., Weisshar,B., Hennig,S., Steinfath,M., and Radelof,U.

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant U. 32 (5), 845-887 (2002)

Contact: Weisshaar B ADIS DNA cential sugar beet genes ADIS DNA cential to a MPIZ MAX-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 bp mRNA linear EST 06-DEC-2002 CDNA clone 024-002-X08-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris BQSBS098 BQSBS098 GI:26114680 EST 05-002-X08 SPST 06-024-002-X08 SPST 06-024-002-X08 SPST 06-024-002-X08 SPST 06-024-002-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X08-02-X0
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Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information can be www-bio.llnl.gov/bbrp/image/image.html
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/tab host="DH10B"
/clone lib="NKIC CGAP Br5"
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Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 22 Std Brror: 0.00
Plate: 2 row: K column: 08
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.6; DB 9;
Pred. No. 6.2e+05;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality Insert Length: 255 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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Best Local Similarity 80.0
Matches 16; Conservative
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AUTHORS
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Mus musculus (house mouse)

Mus musculus

Bukaryota, Matazoa; Chordata, Craniata, Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.

1 (base; 1 to 22)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longadze,S., Mammoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

In Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Bromedical Polymers Research Bidg., 20 S. 2030 E., SLC, UT.
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Kleinwanzlebener Saaczucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not!, primer sites and
                                                                                                                                                                                                                                                                      Orientation:
SP6-Sall-CCACGCGCCCG-Sprime-cDNA-polyA-CC-Notl-77; Note:
SP6-Sall-CCACGCGCCCG-5prime-cDNA-polyA-CC-Notl-77; Note:
Sequencing granted in the context of the GABI-Beet project local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Pred. No. 6.2e+05;
0; Mismatches 5;
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Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0060 row: B column: 11
Seq primer: cGTTGTAAAACGACGGCCAGT
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Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
xref="GABI:181599"
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/strain="C57BL/6J"
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musculus C57BL/6U famile) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a constant velocity. The sheared DNA was blunt end-reparted with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purpired and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi/q73214 gb) high 20/72.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptore complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chanterally-competent E. coli X110-Gold (Stratagene) cells and selected for ampicilin resistance."
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Unpublished
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wannersity of Utah
Hen. 398 Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 22)
1 (bases 1 to 22)
Musculus, Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.8%; Score 13.6; DB 28; Length 22;
80.0%; Pred. No. 6.2e+05;
iive 0; Mismatches 4; Indels
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Insert Length: 10000 Std Brror: 0.00
Plate: 0180 row: E column: 12
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@geneti
Insert Length: 1000
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Best Local Similarity 80.03
Matches 16; Conservative
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                  Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonal excess. The adaptored bnA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ607348 GI:11729538
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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// lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
// clone_lib="Mouse 10kb plasmid UUGCIM library"
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: D column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0429D18"
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Location/Qualifiers
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Mus musculus (house mouse)
Mus musculus
Mus musculus
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Best Local Similarity 80.0°
Matches 16; Conservative
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84112, USA
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/lab host="E. Coli strain XI10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_Tib="Wouse 10kb plasmid UUGCIM library"
/motes=Tvector: PWD42nv. Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/dcouments/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inductable derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (Dasse 1 to 21)

2 (Strent) (Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., and Radelof, U., Entrach, H. and Radelof, U., Merck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U., 32 (S), 845-857 (2002)

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant U. 32 (S), 845-857 (2002)

Contact: Weisshaar B.

ADIS DNA core facility at MPIZ

Max-Plant Little for Plant Breeding Research

Carl-von-Linne Meg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaampiz-Keeln.mpg.de

Insert Length: 21 Scd Error: 0.00

Plate: 19 row: H column: 11

Seg primer: 17, GTAARAGGGCTCACTARAGGGC.
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BQ590339.1 GI:26119922
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/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.9%; Score 13.2; DB 28; Length 21; Best Local Similarity 83.3%; Pred. No. 8.38+05; Matches 15; Conservative 0; Mismatches 3; Indels (
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/lab_host="EMDH108"
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/clone="024-019-H11"
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                                                                                            Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonocleotides were
ligated to the blunt ends in high monlar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agardse gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|A7129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli Xii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                       /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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                'clone_lib="Mouse 10kb plasmid UUGC1M library"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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'clone="UUGC1M0282004"
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Location/Qualifiers
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80.0%;
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Matches 16; Conservative
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BQS91421 21 bp mRNA linear EST 06-DEC-2002 E012714-024-017-P09-T7 MPIZ-ADIS-024-storage root Beta vulgaris CDNA clone 024-017-P09 3-PRIME, mRNA sequence.
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| /clone lib="WPH2ADIS-ADIS-024-storage root" |
| /clone lib="Westor room sugar beet, lib=rary provided by KWS |
| /clone lib="Satistacht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-Notl, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 orientation:
SP6-Sall-CCACGCGCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
SP6-Sall-CCACGCGTCCG-Sprime-context of the GABI-Beet project
Sequencing granted in the context of the GABI-Beet project
, local Pl: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
a 0 c 21 g 0 t
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/culTivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta vulgaris

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae, Beta

(bases 1 to 21)

(bases 1 to 21)

Nervice, Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Brungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
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fingerprinting allows access to 25 000 potential sugar beet genes
fingerprinting allows access to 25 000 potential sugar beet genes
blant J. 32 (5), 485-8857 (2002)

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

ADIS DNA core facility at MPIZ

ANX-Planck Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 0049221562881

Esmail: weisshaadsmpiz-koeln.mpg.de

Insert Length: 21 Std Error: 0.00

Plate: 17 row: P column: 09

Seq primer: T7; ATATAGAGATCACTATAGGGC.
                                                                                                                                                                             Gaps
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database: http://gabi.rzpd.de
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                                                                                                                  Length 21
                                                                                                                                                                          5; Indels
                                                                                                                  Score 13; DB 13;
Pred. No. 9.5e+05;
                                                                                                                                                                             0; Mismatches
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   RZPD/GABI-Primary
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1 Similarity 76.2%;
16; Conservative
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

Caryophyllales; Amaranthaceae; Beta.

(aryophyllales; Amaranthaceae; Beta.

(aryophyllales; Amaranthaceae; Beta.

(brungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Lontact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 0492215062881

Email: weisshaa@mpiz-koeln.mpg.de

Insert Length: 21 Std Error: 0.00

Plate: 17 row: O column: 14

Seq primer: 17; row: O column: 14

Seq primer: 17; row: O column: 14

Seq primer: 17; row: O column: 14
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b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI; primer sites and
orientation:
                                                                                                                                                                       SP6-Sall-CCACGCGTCCG-Sprime.cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GABI-Beet project , local PI: Dr. Katharina Schnëider, coordinator: Prof. CAristian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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BQ591392.1 GI:26120975
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Best Local Similarity 76.21
Best Local 6, Conservative
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BQ591392/c
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1 GGGGGGGGGGGGGGGGG 21

Search completed: October 27, 2003, 13:59:26 Job time: 1847.4 secs

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Sequence 175, App
Sequence 175, App
Sequence 36, Appl
Sequence 73, Appl
Sequence 24, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 13, Appli
Sequence 13, Appli
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Sequence 8, Appli
Sequence 19, Appl
Sequence 19, Appl
Sequence 17, Appl
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Patent No. 5932556
GENERAL INFORMATION:
FAPLICAMT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STREET: California
COUNTRY: United States of America
ZIP: 90631
US-08-886-161-16

US-09-1490-672-35

US-09-194-78-8

US-08-132-575B-19

US-08-199-542B-19

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US-08-85-825-17

US-08-85-825-17

US-08-863-639A-175

US-08-863-639A-175

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US-08-863-639A-175

US-08-863-639A-175

US-08-109-663-639A-175

US-08-109-663-173-1

US-08-109-663-173-1

US-08-109-663-173-1

US-08-109-663-173-1

US-08-103-173-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-5EP-1995
CLASSIFICATION: 424
ATTORNEY/AGBOT INFORMATION:
NAME: Fish, Robert D.
RECISTRATION NUMBER: 33,880
RECISTRATION NUMBER: 33,880
RECISTRATION NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 714-525-3303
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
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Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 204, Appli
Sequence 56, Appli
Sequence 56, Appli
Sequence 56, Appli
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960, 3

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111, Appliant 12, Appliant 12, Appliant 12, Appliant 110, Appliant 110, Appliant 110, Appliant 12, Appliant 12,
                                                                                                                                                                                                                    October 27, 2003, 10:32:34; Search time 48.2 Seconds (without alignments) 192.304 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 2
Sequence 5
Sequence 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-529-878B-4
US-08-529-878B-45
US-08-529-878B-3
US-08-529-878B-3
US-08-529-878B-4
US-08-476-712-2
US-09-471-291-2
US-09-262-773-204
US-08-890-979-56
US-09-032-894-56
US-09-032-894-56
US-09-032-894-56
US-09-032-894-56
US-09-032-888-11
US-08-863-639A-48
US-08-863-639A-48
US-08-863-639A-48
US-08-863-639A-16
US-08-863-639A-16
US-08-863-639A-16
US-08-863-639A-16
US-08-403-888A-117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569978 segs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 nucleic search, using sw model
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21
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8.8.8.8
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Maximum DB
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Gaps
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PARELL INFORMATION:
PARELL INFORMATION:
PAPPLICANT: Tam, Robert C.
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION UNDERSOR OF SEQUENCES:
ADDRESSEE: Crockett & Fish STREET: 3000 S. Augusta Court CITY: La Habra
STREET: 3000 S. Augusta Court CITY: La Habra
CONTRY: California
COMPUTE: California
COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTE: Ploppy disk COMPUTE: Ploppy disk COMPUTE: The PC COMPATION DATA:
MEDIUM TYPE: Floppy disk COMPUTE: 13-SPE-1995
CLASSIFICATION DATA:
PAPPLICATION NUMBER: 33,880
REGISTRATION NUMBER: 33,880
REGISTRATION NUMBER: 33,880
REGISTRATION NUMBER: 33,003
TELLEPHONE: 714-525-3303
TELLEPHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.7%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 58; Matches 18; Conservative 0; Mismatches
            PELECTION NUMBER: US/08/525
FILING DATE: 13-5EP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TTGGAGGGGTGGTGGGG 21
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                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: un
MOLECULE TYPE:
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1 Similarity 100.0%; Score 21; DB 2; Length 21;
21; Conservative 0; Mismatches 0; Indels
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Sequence 3, Application US/08529878B

Patent No. 5932556

GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48

CORRESPONDENCES: 48

COUNTY: La Habra

STATE: 1000 S. Augusta Court

COUNTRY: United States of America
                                                                US-SUB-SUB-45.

Sequence 45, Application US/08529878B
Patent No. 5932556
GENERAL INFORMATION: Robert C.
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION UNMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Crockett & Fish
STREET: 13000 S. Augusta Court
CITY: La Habra
STREET: Galifornia
COUNTRY: United States of America
STREET: United States of America
COUNTRY: United States of America
STREET: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: NEADABLE FORM:
MEDIUM TYPE: NOTAPE: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1955
CLASSIFICATION: 424
ATTORNET/AGENT UNMBER: 33,800
REGISTRATION: WUMBER: 33,800
REGISTRATION NUMBER: 33,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGTTGGAGGGGGTGGTGGGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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Best Local Similarity
Matches 21; Conserva
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Pred. No. 58;

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Gaps
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                 COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: US COMPATIBLE

RELIGIOUS DATE: 04-Oct-1999

CLASSIFICATION CURREN: 08/476,712

RILING DATE: CURROWN-

ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 4;
Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 204, Application US/09262773
Patent No. 622541
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ballinger, Wei
APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONA
TITLE OF INVENTION: SUSCEPTIBLITY GENE CHD1
FILE REPERENCE: Myriad 3 SUSCEPTIBLITY GENE CHD1
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: YUll4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGTTGGAGGGGGTGGTGGG 20
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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80.0%;
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Best Local Similarity 84.2%;
Matches 16; Conservative
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 204
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Best Local Similarity 80.0
Matches 16; Conservative
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CORGANISM: DNA fragment
US-09-262-773-204
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US-09-262-773-204
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US-09-411-291-2
Sequence 2, Application US/09411291
Sequence 2, Application US/09411291
Patent No. 6303376
GENERAL INFORMATION:
APPLICANT: Glazer, Peter, M.
TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
                                                                                                                                                                                                                   Sequence 2, Application US/08476712;
Sequence 2, Application US/08476712;
Patent No. 296246
GENERAL INFORMATION:
TILLE OF INVENTION: Triple-Helix Forming Oligonuclectides for TILLE OF INVENTION: Targeted Mutagenesis
TILLE OF INVENTION: Targeted Mutagenesis
TORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1201 West Peachtree Street
STREET: 1201 West Peachtree Street
STREET: 4 Atlanta
STREET: 4 OLSA
STREET: 4 OLSA
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ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Florpy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,712
FILING DATE: 7-TUNE.1995
CLASSIFICATION: 5.14
ATTORNEY/AGENT INFORMATION:
NAME: PADSE, PATER L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REJERENCE/DOCKET NUMBER: 40114
TELEFRACOMMUNICATION INFORMATION:
TELEFRACOMMUNICATION INFORMATION:
TELEFRACOMMUNICATION INFORMATION:
TELEFRACOMMUNICATION INFORMATION:
TELEFRACOMMUNICATION INFORMATION:
TELEFRACOMMUNICATION INFORMATION:
TELEFRACOMMUNICATION:
TELEFRACOMMUNICATION OF 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
1201 West Paachtree Street
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                                  1 Treckedectereses 18
                                                                       4 TTGGAGGGGGTGGTGGGG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) TOPOLOGY: linear
) MOLECULE TYPE: DNA
US-08-476-712-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
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Gaps
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APPLICANT: Ordovas, Jose M.
TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND TITLE OF INVENTION: CADDIOVASCULAR DISORDERS
FILE REPERENCE: MIA-005.04
CURRENT APPLICATION NUMBER: US/09/031,626
CURRENT FILING DATE: 1998-02-27
EARLIER APPLICATION NUMBER: 08/890,979
BARLIER RILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN Ver. 2.0
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US-09-032-894-56/C
; Sequence 56, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
APPLICANT: Action, Susan L.
TITLE OF INVENTION: SR. BI NUCLBIC ACIDS AND USES THEREFOR
FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT PILING DATE: 1998-02-27
; EARLIER FILING DATE: 1998-07-10
; WUMBER OF SEQ ID NOS: 121
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 56
; SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                           Length 20;
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                                                                                                                                                                                                                                                                                                                                              3; Indels
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83.3%; Pred. No. 4e+03;
tive 0; Mismatches 3;
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Pred. No. 4e+03;
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                             35,430
ER: MIA-005.02
                                          NAME: ARDOIG, Beth E.

REGISTRATION NUMBER: 35,430
REPERRENCE/DOCKET NUMBER: 35,430
RELECOMMUNICATION INFORMATION:
TELEPRAN: 617-832-1000
TELEPRAN: 617-832-1000
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
bESCRIPTION: /desc = "primer"
US-08-890-979-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Application US/09031626
Patent No. 6228581
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENI INFORMATION:
NAME: Arnold, Beth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3
Matches 15; Conservative
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CRGANISM: Human
US-09-032-894-56
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US-09-031-626-56/c
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        Sequence 56, Application US/08890979
Patent No. 6030778
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: Ordovas, Jose M.
TITLE OF INVENTION: DISGRESS
TITLE OF INVENTION: DISGRESS
CORRESSED: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.9%; Score 13.2; DB 2; Length 20; Best Local Similarity 83.3%; Pred. No. 4e+03; Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/890,979
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 US-08-890-980-56/c
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APPLICANT: Reddy, Naeem B.
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: Deprotecting
TITLE OF INVENTION: Deprotecting
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                COMPUTER: IBM
CORPUTER: Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/873,915A
FILING DATE: 19920424
FILING DATE: 19920424
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BUGGOON, Richard P.
REFERENCE/DOCKET NUMBER: 128D-111
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.9%; Score 13; 76.2%; Pred. No.
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2500 Harbor Boulevard
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
  MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
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ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFRENCE/DOCKET NUMBER: 128E
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (714) 773-6971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM
OPERATING SYSTEM: MS.DOS
SOFTWARE: WORDSTEECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/2:
FILING DATE: Unne 8, 1994
CLASSIFICATION: 435
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TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Fullerton
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
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US-07-873-915A-3
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1.026710N: 1..20

2.07HER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complemen

US-09-422-976-9409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET: 020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
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                                                                                                                                                               62.9%; Score 13.2; DB 3; Length 20; 83.3%; Pred. No. 4e+03; Live 0; Mismatches 3; Indels
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APPLICANT: Hanna, Naeem B.
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: for Cleaving and
TITLE OF INVENTION: Deprotecting
TITLE OF INVENTION: Digonucleotides
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSED: BECKman Instruments, Inc.
STREET: 2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9409, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
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Patent No. 5348868
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  3 GTTGGAGGGGGTGGTGGG 20
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                                                                                                                                                               Query Match 62.9
Best Local Similarity 83.3
Matches 15; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Fullerton
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-422-978-9409/c
                                                     TYPE: DNA
CRGANISM: Human
US-09-031-626-56
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US-07-873-915A-3
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SEQ ID NO 56
LENGTH: 20
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US-08-863-639A-11/C
US-08-863-639A-11/C
US-08-863-639A-11/C
Sequence 11, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION.
APPLICANT: Cassin, Peter J.
APPLICANT: Rampel, Jang B.
APPLICANT: Rampel, Jang B.
APPLICANT: Rampel, Jang B.
APPLICANT: Rampel, Jang B.
APPLICANT: Cassey.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES:
STREET: 225 SOUTH Lake Avenue, 9th Floor
CITY: Pasadena
STREET: 225 SOUTH Lake Avenue, 9th Floor
CITY: Pasadena
COMPUTER: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: May 28, 1.997
ATTORING'A ACTORION NUMBER: 20,532
REFERENCE/DORONER: NUMBER: 20,532
REFERENCE/DORONER: 11859-1
TELEFONA: (626) 796-4000
TELEFAX: REPEREDICE CAPER PRICES
TYPE: MUNICE CHARACTERISTICS:
LENGTH TYPE: MULLIPLE CAPER PRICES
TYPE: MULLIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.9%; Score 13; DB 2; Length 21; Best Local Similarity 76.2%; Pred. No. 4.8e+03; Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                    Query Match
61.9%; Score 13; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGTTGGAGGGGGTGGGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGTTGGAGGGGGTGGTGGGG 21
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                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: DNA (genomic)
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                            , ANTI-SENSE: no
US-08-257-964-3
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Search completed: October 27, 2003, 14:03:34 Job time : 48.2 secs

Sequence 20, Appl Sequence 11, Appl Sequence 11, Appl Sequence 30, Appl Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 296, Appl Sequence 296, Appl Sequence 21, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 174, Appl Sequence 16, Appl Sequence 174, Appl Sequence 21, Appl

Sequence Sequence Sequence

Sequence

us-09-331-204a-6.szlm22.rnpb

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US-09-08-4-162A-22/c
| Sequence 22, Application US/09874162A
| Petron No. US-0020155452A1
| GENERAL INFORMATION:
| APPLICANT: ROONEZ, Jason
| APPLICANT: ROONEZ, Jason
| TITLE OF INVENTION: ENDOMERRIAL STROWAL TUMORS
| CURRENT APPLICATION NUMBER: US/09/874,162A
| CURRENT PILING DATE: 2001-06-04
| PRIOR PILING DATE: 2000-06-02
| NUMBER OF SEQ ID NOS: 23
| SEQ ID NOS: 23
| SEQ ID NO 22
| LENGTH NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.4; DB 10;
Pred. No. 2.3e+04;
0; Mismatches 1;
4 US-10-181-846-35
1 US-09-988-115A-33
1 US-09-988-115A-20
2 US-09-9828-034-11
2 US-09-9828-034-10
1 US-09-9828-153-20
1 US-09-9818-875-295
1 US-09-9818-875-295
1 US-09-9818-875-295
1 US-09-9818-875-295
1 US-09-9818-875-295
1 US-09-9818-893-174
1 US-09-9918-696-23
1 US-09-9918-696-23
1 US-09-9918-696-23
1 US-09-9918-696-23
1 US-09-9918-696-23
1 US-09-9918-696-23
1 US-09-998-003-133
0 US-09-985-003-133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: primer for PCR US-09-874-162A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.3%; Pr
Matches 14; Conservative 0;
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ORGANISM: Artificial Sequence
FEATURE:
    6 GGAGGGGGTGGTGGG 20
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    000000000000
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US-09-779-152-56/c
    Sequence 22, Appl
Sequence 56, Appl
Sequence 513, Appl
Sequence 2133, Ap
Sequence 2422, Ap
Sequence 2422, Ap
Sequence 2423, Appl
Sequence 26, Appl
                                                                                           October 27, 2003, 11:25:34; Search time 452.6 Seconds (without alignments) 124.432 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*

| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USOF_PUBCOMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-779-152-56
US-09-740-332-2132
US-09-740-332-2132
US-09-740-332-2133
US-09-740-332-2422
US-09-817-879-2133
US-09-817-879-2133
US-09-817-879-2422
US-09-817-879-2422
US-09-828-034-2422
US-09-828-034-2423
US-10-059-888-26
US-10-303-108A-30
US-10-303-108A-30
US-10-204-888-56
                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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21
1 999ttggaggggtggtggtgg 21
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Gapop 10.0 , Gapext 1.0
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length: 22
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Match
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Maximum DB seq
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Gaps

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Indels

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Sequence 2422, Application US/09740332
Sequence 2422, Application US/09740332
Publication No. US20030125270A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FILE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPREMENT APPLICATION NUMBER: US/09/740,332
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 2422
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2133, Application US/09740332

Sequence 2133, Application US/09740332

Publication No. US20030125270A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003

FILE REFERENCE: RPI 400/003

CURRENT APPLICATION UNMERS: US/09/740,332

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9704

SOFTWARE: ParentIn version 3.0
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Pred. No. 3.3e+04;
0; Mismatches 0; Indels
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                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION:
TOCATION:
FORTION:
COTTER INFORMATION: oligonucleotide substrate
US-09-740-332-2132
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// LOCATION:

// OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-2133
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Best Local Similarity 100.0%; P
Matches 13; Conservative 0;
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ORGANISM: artificial sequence
FEATURE:
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     TYPE: RNA ORGANISM: artificial sequence
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Best Local Similarity 100.0
...hes 13; Conservative
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US-09-740-332-2422
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LENGTH: 17
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US-09-740-332-2132/c
US-09-740-332-2132/c
SQUENCE 2132, Application US/09740332
FUBLICATION NO. US20030128270A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION WUMBER: US/09/740,332
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOUTWARE: Patentin version 3.0
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APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
TITLE OF INVENTION: DAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
FILE REFERENCE: MMI-1720P2
CURRENT APPLICATION NUMBER: US/09/779,152
CURRENT APPLICATION NUMBER: US/09/779,152
PRIOR APPLICATION NUMBER: 08/890,979
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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APPLICANT: Acton, Susan L.

TITLE OF INVENTION: SR-BI NUCLBIC ACIDS AND USES THEREFOR FILE REFREENCE: MIA-005.03

CURRENT APPLICATION NUMBER: US/10/023,610

CURRENT FILING DATE: 2001-12-17

EARLIER APPLICATION NUMBER: 09/686,106

EARLIER FILING DATE: 2000-10-10

EARLIER FILING DATE: 1998-02-27

EARLIER FILING DATE: 1998-02-27

EARLIER FILING DATE: 1998-02-27

MUMBER OF SEQ ID NOS: 121

SOFTWARE: PATCHAIL Ver. 2.0

SEQ ID NO 56

LENOTH: 20
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Pred. No. 2.7e+04;
0; Mismatches 3;
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83.3%;
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Best Local Similarity 83.38
Matches 15; Conservative
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US-10-023-610-56
                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-779-152-56
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US-10-023-610-56/c
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Sequence 2422, Application US/09817879

Publication No. U520030171311A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Hepatitis C Virus Infection

FILL REPRENCE: MBHB00-801-7

CURRENT APPLICATION WNBER: US/09/817,879

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9703

SOOTHWARE: Parentin version 3.0

SEQ ID NO 2422

LENGTH: 17
                                 Sequence 2133, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bazymatic Nucleic Acid Treatment of Diseases or Conditions Relat TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPREMENCE: MHBMOO-801-F
CURRENT APPLICATICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2133
LENGTH: 17
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Publication No. US20030171311A1
CENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Brzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MRHB00-801-F
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COTHER INFORMATION: Oligonucleotide substrate US-09-817-879-2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: oligonucleotide substrate US-09-817-879-2422
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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Matches 11; Conserv
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US-09-817-879-2423
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US-09-817-879-2422
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APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPRENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                US-09-140-332-2423
Sequence 2423, Application US/09740332
Sequence 2423, Application US/09740332
Sequence 2423, Application US/09740332
Sequence 2423, Application US/030125270A1
Sebilication No. US20030125270A1
GENERAL INFORMATION:
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
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Query Match 61.9%; Score 13; DB 11; Length 17; Best Local Similarity 84.6%; Pred. No. 3.38+04; Matches 11; Conservative. 2; Mismatches 0; Indels
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Pred. No. 3.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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Publication No. US20030171311A1
GENERAL INFORMATION:
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 100..
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                                                                                               9 GGGGGTGGTGGGG 21
                                                                                                                                           GGGGGUGGUGGGG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2423
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
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Sequence 26, Application US/10059888

Publication No. US203002586241

GENERAL INFORMATION:

APPLICANT: CHAO, LEE

APPLICANT: CHAO, JULIE

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING

TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL

TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL

TITLE OF INVENTION: 17550E KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL

TITLE OF INVENTION: 10913.0081U2

CURRENT APPLICATION NUMBER: 09/495,140

PRIOR FILING DATE: 2000-01-31

PRIOR APPLICATION NUMBER: 09/389,566

PRIOR APPLICATION NUMBER: 08/389,566

PRIOR APPLICATION NUMBER: 08/389,566

PRIOR APPLICATION NUMBER: 08/386,141

PRIOR FILING DATE: 1997-05-14
                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490Ale = , OTHER INFORMATION: synthetic construct
US-10-059-877-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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US-10-303-1094-30/C
| Sequence 30, Application US/10303109A
| Sequence 30, Application US/10303109A
| Sequence 30, Application US/20030194726A1
| GENERAL INFORMATION:
| APPLICANT: BOLCHAKOVA, Elena
| APPLICANT: CONTENT OF THE 1700 STORT |
| CURRENT FILING DATE: 2002-11-22
| PRIOR APPLICATION NUMBER: US 60/334,798
| PRIOR FILING DATE: 2001-11-30
| NUMBER OF SEQ ID NOS: 39
| SEQ ID NO 30
| LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match.
61.0%; Score 12.8; DB 12;
Best Local Similarity 87.5%; Pred. No. 4e+04;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.0%; Score 12.8; DB 12;
87.5%; Pred. No. 4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
            PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 08/856,141
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 17
                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GGAGGGGGTGGTGGGG 21
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Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Thermus oshimai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-303-109A-30
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Publication No. US20030157490A1
GENERAL INFORMATION:
APPLICANT: CHAO, LEE
APPLICANT: CHAO, JULIE
APPLICANT: SONG, QING
TITLE OF INVENTION: MFPERTENSION
TITLE OF INVENTION: HFPERTENSION
TITLE OF INVENTION: HFPERTENSION
CURRENT APPLICATION NUMBER: US/10/059,877
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 09/495,140
PRIOR APPLICATION NUMBER: 09/495,140
PRIOR APPLICATION NUMBER: 09/389,566
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-31
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13; DB 12; Length 1/
Pred. No. 3.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09828034
Patent No. US20020064771A1
GENERAL INFORMATION:
APPLICANT: Anong, Weidong
APPLICANT: Hong, Zhi
APPLICANT: Hong, Zhi
APPLICANT: Hong, Zhi
TITLE OF INVENTION: HCV REPLICASE COMPLEXES
FILE REFERENCE: IN01165
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION:
1 O'THEN O'THEN O'THEN O'THEN O'S O'THEN O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SSOFTWARE: Patentin version 3.0
LENGTH: 17
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                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
SEQTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 GGGGGTGGTGGGG 21
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US-09-828-034-31/c
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US-10-059-877-26
                                                                                                                                                                                                                                                                                                            FEATURE:
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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030025882Ale = ; OTHER INFORMATION: synthetic construct
US-10-059-888-26
                                                                                                                                                                                                                                                Query Match 61.0%; Score 12.8; DB 14; Length 17; Best Local Similarity 87.5%; Pred. No. 4e+04; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps
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Search completed: October 27, 2003, 19:00:53 Job time : 453.6 secs

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Run on:

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cgn2 6 (prodata/1) pna/US101B COMB seq:
cgn2 6 (prodata/1) pna/US5001 COMB seq:
cgn2 6 (prodata/1) pna/US5002 COMB seq:
cgn2 6 (prodata/1) pna/US5002 COMB seq:
cgn2 6 (prodata/1) pna/US5003 COMB seq:
cgn2 6
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1: \( \text{cgn2} \) \( \text{fytodata} \) \( \text{fytodata}
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33363688 segs, 16581889874 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                       US-09-331-204A-6
21
1 999ttggagggggtggtgggg 21
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seg length: 0
seg length: 22
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                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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Maximum DB
                                                                                                                                             OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli
SU ID	8 US-08-387-041A-4 19 US-09-331-204-6 19 US-09-331-204A-6 8 US-08-387-041A-3
В	9 7 9
% Query Match Length DB	21 21 21 18
% Query Match	21 100.0 21 100.0 21 100.0 18 85.7
Score	1 21 100.0 21 2 21 100.0 21 3 21 100.0 21 4 18 85.7 18
kesult No.	

us-09-331-204a-6.szlm22.rnpm

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REFERENCE/DOCKET NUMBER: 8250
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 66141 PENNE
INFORMATION PEN SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           JOYULOGY: UNKNOWN
; MOLECULE TYPE: DNA (genomic)
US-08-387-041A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                         LEANSTICS:
LOANTH: 21 Dass pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
OLEGIT F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-331-204A-6
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Matches
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Sequence 2660, Ap
Sequence 2660, App
Sequence 2660, App
Sequence 2660, App
Sequence 3940, A
Sequence 63940, A
Sequence 1878, A
Sequence 17426, A
Sequence 47426, A
Sequence 47426, A
Sequence 47426, A
Sequence 47426, A
Sequence 4185, A
Sequence 4353, A
Sequence 4353, A
Sequence 18418, A
Sequence 3562, A
Sequence 3562, A
                        Sequence 4, Appli
Sequence 17, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 17, Appli
Sequence 17, Appl
Sequence 218, Appl
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GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
TITLE OF INVENTION: OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
9 US-09-331-2044-1
3 US-09-331-2044-4
3 US-09-331-2044-4
9 US-09-331-2044-8
9 US-09-331-2044-8
9 US-09-331-2044-8
9 US-09-331-2044-9
0 US-09-331-204-9
0 US-09-435-6
0 US-10-206-090-435-6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/387,041A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CUUNIRY: United States of America
21P: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
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US-08-387-041A-4
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Sequence 6, Application US/09331204A
Sequence 6, Application US/09331204A
GENERAL INFORMATION:
APPLICANT: TOR PHARMECULICALS, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Rest
TITLE OF INVENTION UNMER: US/09/331,204A
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT PILING DATE: 1999-08-20
CURRENT PILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 28
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tam, Robert
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: IMMUNE RESPONSE
TITLE OF INVENTION: IMMUNE RESPONSE
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT APPLICATION NUMBER: US/09/331,204
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR PELLING DATE: 1999-08-20
PRIOR PELLING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: An oligomer, OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic OTHER INFORMATION: acid. This term includes oligomers consisting of OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 19; Length 21; larity 100.0%; Pred. No. 1.18+03; Conservative 0; Mismatches 0; Indels
                               Length 21;
                                                              1e+03;
                           Score 21; DB 8;
Pred. No. 1.1e+03
                                                                                      Mismatches
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                                                                                                                                              1 GGGTTGGAGGGGGTGGGG 21
                                                                                                                                                                                                   1 GGGTTGGAGGGGGTGGTGGGG 21
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APPLICANT: Tam, Robert
Ouery Match
Best Local Similarity 100.0%; Pr
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PCT/US97/23927
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US-09-786-436-17
Sequence 17, Application US/09786436
, GENERAL INFORMATION:
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Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
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PRIOR APPLICATION NUMBER: PCT/US
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 TTGGAGGGGGTGGTGGGG 21
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CRGANISM: synthetic construct
US-09-331-204A-4
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SEQ ID NO 4
LENGTH: 18
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US-09-331-204-1
; Sequence 1, Application US/09331204
; Sequence 1, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; TITLE OF INVENTION: INMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
TITLE OF INVENTION: OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
                                                                                           Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
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ZIP: 10036
COMPUTER ENDABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: Propry disk
COMPUTER: Propry disk
COMPUTER: PROPED COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,041A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8250-011
TELEPHONION: 415-854-3660
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3660
TELEFAX: 415-854-3660
TELERATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TEMBORMATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                           Score 21; DB 19;
Pred. No. 1.1e+03;
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85.7%; Score 18; DB

Best Local Similarity 100.0%; Pred. No. 1.2

Matches 18; Conservative 0; Mismatches
                                                                                                                                     0; Mismatches
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                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative 0
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MOLECULE TYPE: DNA (genomic)
  ; TYPE: DNA; ORGANISM: synthetic construct US-09-331-204A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: unknown
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US-08-387-041A-3
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TCM. Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
ITILE OF INVENTION:
GENERAL OF INVENTION:
GENERAL OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 216/013-019.
CURRENT PELLING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: BCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PT-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
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OTHER INFORMATION: Description of Artificial Sequence: An oligomer, OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic, OTHER INFORMATION: acid including oligomers consisting of naturally, OTHER INFORMATION: occurring bases, sugars and intersugar US-09-331-204-1
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APPLICANT: Lipford, Grayson
APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Mocif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: C1041/7010 (AMS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/EP99/06502
PRIOR APPLICATION NUMBER: PCT/EP99/06502
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 19; I 
Pred. No. 1.2e+04;
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Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0;
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Sequence 7, Application US/09331204A
GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
APPLICANT: 1897-1031, 204A
CURRENT APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
NUMBER: Patentin version 3.0
SOUTWARE: Patentin version 3.0
                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: 1CO Pharamaceuticals, Inc.
APPLICANT: TCO Pharamaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resp.
FILE REPERENCE: 216/013-021
CURRENT FALLING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
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     Indels
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Pred. No. 4.5e+04;
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Pred. No. 1.7e+05;
0; Mismatches 2;
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     Mismatches
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                                                   4 TTGGAGGGGTGGTGGGG 21
                                                                                                 1 TTGGAGGGGAGGTGGGG 18
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; ORGANISM: synthetic construct
US-09-331-204A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TTGGAGGGGGTGGTGGGG
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     17; Conservative
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SOFTWARE: P:
SEQ ID NO 8
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     Matches
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TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN TITLE OF INVENTION: IMMURE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR PILING DATE: 1999-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver: 2.0
SOFTWARE: PatentIn Ver: 2.0
SOFTWARE: PATENTIAL SEQUENCE
TYPE: DA
TYPE: DA

ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence: An oligomer
OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
OTHER INFORMATION: acid. This term includes oligomers consisting of
OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-5)
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                                                                                                 Length 18;
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                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Information APPLICANT: Inford, Grayson APPLICANT: Heeg, Klaus APPLICANT: Heeg, Klaus TITLE OF INVENTION: G-Mocif Cligonucleotides and Uses TITLE OF INVENTION: Thereof FILE REFERENCE: Clo41/7010 (AMS) CURRENT APPLICATION NUMBER: US/09/786,436 CURRENT FILING DATE: 2001-03-02 PRIOR APPLICATION NUMBER: PCT/EP99/06502 PRIOR FILING DATE: 1999-09-03 NUMBER OF SEQ ID NOS: 42 SOFFWARE: FastSEQ for Windows Version 3.0
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85.7%; Score 18; DB 33; I
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0;
                                                                                           Query Match
85.7%; Score 18; DB 33; ...
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0;
; FEATURE:
. OTHER OLIGONATION: Synthetic oligonucleotide
US-0786-436-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-786-436-42/c
; Sequence 42, Application US/09786436
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09331204 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-331-204-5
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LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Tam, Robert
TITLE OF INVENTION: GENERAL INFORMATION:
TITLE OF INVENTION: GENERAL INFORMER: AND METHODS OF MODULATING AN TITLE OF INVENTION: INFORMER: US/09/331,204
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PS9-12
PRIOR APPLICATION NUMBER: PS7-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: An oligomer OTHER INFORMATION: or polymer of ribonucleic acid or decyribonucleic OTHER INFORMATION: acid. This term includes oligomers consisting of OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
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US-10-303-778-3043
US-10-303-778-3043, Application US/10303778
; GEQUENCE 3043, Application US/10303778
; GENERAL INFORMATION:
    APPLICANT: ROSettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: Patentin version 3.1
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70.5%; Score 14.8; DB 19;
Best Local Similarity 88.9%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 18
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                                                                                                                                                                                                      TYPE: DNA; ORGANISM: synthetic construct US-09-331-204A-9
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTGGAGGCGGTGGTGGCG
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CORGANISM: Homo sapiens
US-10-303-778-3043
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LENGTH: 22
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LENGTH: 19
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DEFINITION TO SECULATE TO SECULATE THE SECULATORY OF NOVEL VIRAL REGULATORY GENTITLE OF INVENTION: USES THEREOF TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 47487 CURRENT APPLICATION NUMBER: US/10/310,188 CURRENT FILING DATE: 2002-12-19 NUMBER OF SEQ ID NOS: 86841 SOFTWARE: PATENTIN VERSION 3.1
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Score 14.8; DB 50; Length 22; Pred. No. 1.6e+05; O; Mismatches 2; Indels
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Pred. No. 1.9e+05;
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                                                                                                                                                                                         ; Sequence 41819, Application US/10310188 ; GENERAL INFORMATION:
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81.0%; Pred
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 70.5%;
88.9%;
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Best Local Similarity 81.0
Matches 17; Conservative
                Best Local Similarity 88.9
Matches 16, Conservative
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US-10-310-188-41819
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US-10-310-188-41819
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LENGTH: 21
 Query Match
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RESULT 2
PCT-US02-38216-51871
Sequence 51871, Application PC/TUS0238216
GENERAL INFORMATION:
TOTAL OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENERAL POTT/US02/38216
TITLE OF INVENTION: GENERAL PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT PILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 22
LENGTH: 22
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GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: GENER AND USES THEREOF
TITLE OF INVENTION: GENER AND USES THEREOF
FILE REFERENCE: 55002
CURRENT PILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSPTWARE: Patentin version 3.2
SEQ ID NO 41819
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    Sequence 29535,
Sequence 51842,
Sequence 61077,
Sequence 86378,
Sequence 6852,
Sequence 6852,
Sequence 6852,
  Sequence 39492,
Sequence 57248,
Sequence 38927,
Sequence 38577,
Sequence 55622,
Sequence 57624,
Sequence 5764,
Sequence 6731, A
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29535,
51842,
51896,
61077,
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PCT USO2 38216 - 57248
PCT USO2 38216 - 38927
PCT USO2 38216 - 58927
PCT USO2 38216 - 58927
PCT USO2 38216 - 58927
PCT USO2 38216 - 5862
PCT USO2 38216 - 5884
PCT USO2 38216 - 6885
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Pred. No. 1.5e+04;
); Mismatches 4;
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69.5%; Score 14.6; DB 1;
Best Local Similarity 81.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 4;
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81.0%;
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    TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-41819
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Best Local Similarity
Matches 17; Conserv
    RESULT 1
PCT-US02-38216-41819
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21871, A
21346, A
38943, A
46976, A
26889, A
78689, A
78689, A
78681
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/cgn2 6/ptodata/1/pna/USO7_NEW_COMB.seq:*
/cgn2 6/ptodata/1/pna/USO7_NEW_COMB.seq:*
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/cgn2 6/ptodata/1/pna/USO0_NEW_COMB.seq:*
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(c) 1993 - 2003 Compugen Ltd.
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PCT-USO2-38216-468976
PCT-USO2-38216-468976
PCT-USO2-38216-78687
US-09-978-333B-2
PCT-USO2-38216-78687
US-09-978-333B-2
PCT-USO2-38216-78697
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PCT-USO2-38216-55899
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PCT-USO2-38216-72899
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
FILLE OF INVENTION: GENES AND USES THEREOF
FILLE SPERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION DATE: 2002-11-12
NUMBER: OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
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) GBNERAL INFORMATION:
APPLEANT: ROSetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BIOINFORMATICALLY
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larity 93.6%; Pred. No. 1.8e+04;
Conservative 0; Mismatches 1; Indels
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Pred. No. 1.8e+04;
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Pred. No. 1.8e+04;
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93.8%;
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Best Local Similarity 93.8%;
Matches 15; Conservative (
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Best Local Similarity 93.8
Matches 15; Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-26689
                                      ORGANISM: Homo sapiens
PCT-US02-38216-38943
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Matches 15; Conserv
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LENGTH: 19
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; TYPE: DNA
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SEGNERAL INFORMATION:
APPLICANT: ROSELTA Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT FILING DATE: 2002-11-12
SOFTWARE OF SEQ ID NOS: 86841
SOFTWARE: Pacentin version 3.2
LENGTH: 19
                                                                                                                                                                                                                      Sequence 2335, 4, Application PC/TUS0238216
SEGNERAL INFORMATION:
APPLICANT: ROSELTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REPERENCE: 55002
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 27376
LENGTH: 18
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GENERAL INFORMATION:
APPLICANT Rosette denomics LTD
APPLICANT Rosette denomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REPERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 8641
SOFTWARE: PATENTIN Version 3.2
SOFTWARE: PATENTIN Version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.4; DB 1; Length 18; Pred. No. 1.8e+04; 0; Mismatches 1; Indels
   GGGTTGGAGGGGGTGGTGGGG 21
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93.8%;
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Best Local Similarity 93.83
Matches 15, Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-27376
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PCT-US02-38216-41647
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PCT-US02-38216-41647
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LENGTH: 18
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Sequence 2, Application US/09978333C
Sequence 2, Application US/09978333C
Sequence 2, Application US/09978333C
Sequence 2, Application Set 2001-10-16
FILE REFERENCE: VU 132
CURRENT APPLICATION NUMBER: US/09/978,333C
CURRENT FILING DATE: 2001-10-15
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 2
LENGTH: 20
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
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Pred. No. 2.1e+04;
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84.2%; Pred. No. 2.1e+04;
tive 0; Mismatches 3;
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TITLE OF INVENTION: BIOINDORMATICALLY DETECTA,
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION WUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 21
      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide AG20
US-09-978-333C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 51847, Application PC/TUS0238216; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
         16; Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-51847.
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US-09-978-333C-2
         Matches
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IIILE OF INVENTION: Triple-Helix forming Oligonucleotides for Targeted Mutagenesis FILE REFERENCE: YU 132
FILE REFERENCE: YU 132
CURRENT APPLICATION NUMBER: US/09/978,333B
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 09/411,291
PRIOR APPLICATION NUMBER: US 08/476,712
PRIOR PILING DATE: 1999-10-04
PRIOR PILING DATE: 1995-10-07
PRIOR PILING DATE: 1995-10-07
SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILL REFERENCE: 55002
FILL REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NOVEL: DCT/US02/38216
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VERSION 3.2
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Pred. No. 2.1e+04;
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Pred. No. 2.1e+04;
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TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 42141
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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CORGANISM: Homo sapiens
PCT-US02-38216-78687
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Best Local Similarity
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LENGTH: 19
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                                                                                                                                                                        TYPE: DNA
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Matches
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Search completed: October 27, 2003, 18:22:55 Job time : 358.2 secs

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Sequence 27360, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT ROSECTE Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 5502
CURRENT APPLICALION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 19
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APPLICANT: ROSELTA GENOMICS LTD

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 5500

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT PILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SEQ ID NO 63940

LENGTH: 22

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                                                                                                                                                                                                                                                                     Query Match 67.6%; Score 14.2; DB 1; Length 21; Best Local Similarity 84.2%; Pred. No. 2.1e+04; Matches 16; Conservative 0; Mismatches 3; Indels
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FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 55389
LENGTH: 21
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GENERAL INFORMATION:
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                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-55389
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PCT-US02-38216-63940
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PCT-US02-38216-27360
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PCT-US02-38216-63940
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PCT-US02-38216-27360
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October 27, 2003, 10:32:29 ; Search time 376.114 Seconds (without alignments) 1957.844 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1. 90-ba: *

3. 90-htg: *

3. 90-pa: *

90-p
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES	ΩI	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4.0	ω, r	9	42	42	4. 4	4 0	1 6	42	42	30	9	9	4. z	1, 4, U RJ	4.2	42	0 4	77	45	AX037374	15	0.7	55	56	57	58	159	27.	A12052	AX729881	2 4	132	324	9 6	AR237949	ALIGNMENTS	21 bo DNA	agnosis primer.	_			<pre>lgnier,L. s of retroviral g for the amplific for the amplific</pre>
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PD 04-APR-2000
PP 24-SBP-1999 JP 1999270165
PR 24-SBP-1999 JP 89/0734,20-SEP-1989 FR 89/12371 PI
PP 24-SBP-1999 JP 89/0734,20-SEP-1989 FR 89/12371 PI
MAURICE MONCANY,LUC MONTAGNIER
PC C12N15/09,A61K39/21,A61K48/00,A61P31/18,C07H21/04,C07K14/155,PC C07K14/16,
PC C12Q1/68,C12Q1/70,G01N33/569,C12N15/00
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PT source Location/Qualifiers
FT Fource / /organism='Artificial Sequence'.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism='Artificial Sequence'
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                                                                                                                                                                                                  / organism="synthetic construct"
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/db_xref="taxon:32630"
a 2 c 13 g 1 t
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Patent: EP 1239051-A 1934 11-SEP-2002;
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Sequence 1934 from Patent EP1239051.
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/mol_type="genomic DNA"
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Unclassified.

(CE 1 (bases 1 to 21)

NS Moncany, M. and Montagnier, L.

Nucleotide sequences derived from the genome of retroviruses of the HIV-1, HIV-2, and SIV type, and their uses in particular for the amplification of the genomes of these retroviruses and for the in viro diagnosis of the diseases due to these viruses

NNAL Patent: US 6194142-A 45 27-FEB-2001;

Location/Qualifiers

Location/Qualifiers
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BD001798.1 GI:16626357
JP 2000093187-A/45.
Synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 21)
Moncany, M. and Montagnier, L.
Immunogenic compounds containing a translation product of
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Patent: JP 2000093187-A 45 04-APR-2000;
INST PASTEUR, INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL
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PN JP 2000093187-A/45
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Patent: EP 0403333-A 29 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE
MEDICALE (INSERM)
Location/Qualifiers
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94.1%; Pred. No. 2.7e+04;
ive 0; Mismatches 1;
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G-mcrif oligonucleotides and uses thereof
Patent: WO 014217-A 42 16-MR-2000,
LIPPORD GRAYSON B (DB) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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Wang,C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 127 19-JAN-1999;
Location/Qualifiers
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0 0 13 9 4 t
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G-motif oligonucleotides and uses thereof
Patent: WO 0014217-A 17-16-MAR-2000,
LIPFORD GRAYSON B (DE); HEEG KLAUG (DE); WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
LOCATION/Qualifiers
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100.0%; Pred. No. 4.2e+04;
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Shannon,M.

Human posh-like protein 1

Patent: EP 1239051-A 1935 11-SEP-2002;

Aeomica, Inc. (US)

Location/Qualifiers
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Patent: EP 1239051-A 1936 11-SEP-2002,
Aeomica, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         Sequence 1936 from Patent EP1239051. AX532427. GI:25256629
                                                                           / Organism="Homo sapiens"
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Sequence 17 from Patent WO0014217.
AX023402.
AX023402.1 GI:10183802
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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| Similarity 100.0%; Pi
| 15; Conservative 0;
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AX532427/c
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
nego gene expression
RIBOTME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
                                                                                               Unaclassified.
Unclassified.
MoKay, R., Freier, S.M. and Wyatt, J.
Antisense modulation of casein kinase 2-alpha prime expression
Patent: US 6455307-A 93 24-SEP-2002;
Location/Qualifiers
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88.2%; Pred. No. 1.38+05;
cive 0; Mismatches 2; Indels
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/mol_tvpe="nena"

/db_xref="taxon:12630"

/noTe="Nucleic Acid"

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Sequence 93 from patent US 6455307.
AR232303.1 GI:27274295
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Sequence 47 from Patent WO0159103.
AX214605
AX214605.1 GI:15524648
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Sequence 46 from Patent WO0159103.
AX214604
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/organism="unknown"
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AX214605/c
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: EP 123905-A 1933 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1239051-A 1937 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 1937 from Patent EP1239051.
AX532428 GI:25256631
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EP1239051.
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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a 12 c 1 g
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Sequence 1933 from Patent
AX532424
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 GGAGGGGGAGGAGGGG 18
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AX532424/c
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 899 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 47 16-AUG-2001;
RIBOYME PARAMACEUTICALS, INC. (US); Blatt, lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 0; Indels
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AZ345792 IM0080G12

AZ760597 IM0554N21

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AZ659755 IM0518210

AZ772707 IM0583118

AZ772707 IM0583118

AZ583408 IM0378N23

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AZ971409 ZM0184E16

AZ976712 ZM0184E16

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qu76g01.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032 3'
similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 19)
NCI/MINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/ETGAP), Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown library type
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
1. 19
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AZ969578
AZ307952
                                                                                                                 AZ331988
AZ607348
AZ645874
AZ871408
AA996014
                                                                                                                                                       AZ397469

AZ31600

AZ36836

AZ366712

AZ366712

AZ38420

AZ394677

AZ394677
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AA968729
         AZ760597
AZ786308
                                                     AZ969440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                           AI251781
AI251781.1 GI:3848310
  Homo sapiens (human)
  Homo sapiens
 RESULT 1
AI251781/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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AI257923 2M0192D07
AIS82080 ar96b07.X
AZ468862 1M0282004
                                                     2003, 10:32:29 ; Search time 1581.77 Seconds (without alignments) 276.576 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
         5.1.6
Compugen Ltd.
                                                                                                                                        22781392 segs, 12152238056 residues
                                                                                                                                                        hits satisfying chosen parameters:
         GenCore version (c) 1993 - 2003
                                                                                                                                                                                                              summaries
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AI582080
AZ468862
                                      nucleic search, using sw model
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                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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                Copyright
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13.8
13.2
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Perfect score:
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Total number Minimum DB s Maximum DB s

Database

1 2 E 4

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Searched:

Sequence:

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/tissue_type="tumor,5" pooled (see description)"
/lab_host="DH108"
/clonellib="NCI_CAAP_BENTS"
/note="Organ: brain, Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: property organization" organization organization" organization organiza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ876923 22 bp DNA linear GSS 21-FEB-2001 2M0192D07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0192D07 F, genomic survey sequence.
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/63 (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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88.2%; Pred. No. 5.5e+05;
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Insert Length: 10000 Std Error: 0.00
Plate: 0192 row: D column: 07
Seq primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1978032"
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University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
Email: ddunn@genet
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was blunt end-repaired with T4 DNA polymerase and T4 polymerase thase. Adaptor oligomerase and T4 ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheard, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ar96b07.x1 Barstead colon HPLRB7 Homo sapiens CDNA clone IMAGE:2173429 3' similar to SW:FOR4_MOUSE Q05859 FORMIN 4 ;contains Al582080.1 GI:4567977
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Conteact: Wilson KY
Washington University School of Medicine
(A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tal: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Thace considered overall poor quality
Possible reversed clone: similarity on wrong strand,
Seq primer: -400F from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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Hillier,L., Allea,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,V., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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/db_xref="taxon:9606"
/clone="IMAGE:2173429"
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Homo sapiens
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AIS82080/c
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us-09-331-204a-8.szlm22.rst

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/ab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone_lib="Wouse_10kb_plasmid_UUGCIM_library"
/note="Westor: PWD42nv; Purified_genomic_DNA_from M.
musculus_C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse_DNA_Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
was hydrodynamically sheared by repeated passage through a
was blunt end-repaired with T4_DNA_polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophores.s. Wector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ345792 19 bp DNA linear GSS 29-SEP-2000 1M0080G12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080G12 R, genomic survey sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 19)
Dun,D., Aoyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Island,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
Mouse whole genome scaffolding with paired end reads from 10kb
Unpublished
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                    Gaps
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                  Score 13.2; DB 28;
Pred. No. 8.3e+05;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 12
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/mol_type="genomic DNA"
/errain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0080G12"
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Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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                                                                                                                                                                                                                                                                                                                                        15; Conservative
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84112, US
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Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 21)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Rome Center
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      [5. AATTCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
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Insert Length: 10000 Std Error: 0.00
Plate: 0282 row: O column: 04
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
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Fax: 801 585 7177
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84112, USA
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                   with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored weter of volumed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
inducible derivative of plasmid R1. The vector was ligated
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Monse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/note="Vector: PWD42ry' Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Unpublished B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Pm. 308, Biomedical Polymers Research Bldg., 20 (
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 19.
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Mus musculus
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AZ760597.1 GI:12868613
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                                                                                                                                                                                                                                                                                                                                             sex="Male"
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Matches 14; Conservative
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of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through (
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was puntified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

(bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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Contact: Robert B. Weise
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42Dry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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Length: 10000 Std Error:
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Fax: 801 585 7177
Email: ddunn@genet
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Gaps

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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|472114 gi), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and elected for ampicillin resistance."
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Mus musculus
Bukaryota;
Mus musculus
Bukaryota;
Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
181am,M., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
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University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                                                                                                                                                                                                             Length 20;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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Unpublished
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Best Local Similarity
Matches 14; Conserv
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and slected for ampicillin resistance."
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Mus musculus

Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Banamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 20)

Munn, D., Advagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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1M0357118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0357118 R, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.1e+06;
0; Mismatches 2; Indels C
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0357118"
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GSS.
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Matches 14; Conservative C
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAS (gi[47221072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0537 row: F column: 22
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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clone="UUGC1M0537F22"
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Location/Qualifiers
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Mus musculus
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophores. Wector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The Vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0583L18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0583L18 R, genomic survey sequence.
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 20)
Dunn, D., Adyagi, Barber, M., Beacorn, T., Duval, S., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rry, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0583 row: L column: 18
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0583L18"
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Fax: 801 585 7177
Email: ddunn@genet
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was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732.14 gbl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus (house mouse)

ISM wis musculus (house mouse)

Mus musculus metazoa, Chordata, Craniata, Verrebrata, Euteleostomi;

Eukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.

ICE (hases 1 to 21)

NS Jan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen T., Reilly, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

NAL Uppublished

Contact: Robert B. Weiss

I University of Utah Genome Center
University of Utah Genome Center
University of Utah Research Bldg., 20 S. 2030 E., SLC, UT

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK476392 1000 21 bp DNA linear GSS 04-OCT-2000 1M0295F12F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0295F12 F, genomic survey sequence. AZ476392
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Tel. 1015 585 5006
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0295 row: F column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
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/clone="UUGC1M0295F12"
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (eig+473.114 | gip|AR12.3072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse_10kb plasmid UUGC2M library"
hote="Vector: PWD42nv; Purified genomic DNA from M.
musculus CS7BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 042 zow: O column: 12
Seg primer: cGTTGTAAAA.GGAGGCCAGT
Class: plasmid ends
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/strain="C57BL/60"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymes and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purpled and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|API29072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Dn. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mus musculus
Mus metazoa; Chorata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chorata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)
Dunn, D., Aoyagi, S., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42ry, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunagenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0527 row: G column: 11
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
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/mol_type="genomic DNA"
farain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIN0527G11"
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  was blunt end-repaired with T4 DNA polymerase and T4 lighted to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarces gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampidillin resistance."
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn, D., Aoyad; A.)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kbr plasmid inserts
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Fax: 801 585 7177

Email: ddunngenetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0378 row: N column: 23

Seq primer: GTTGTAAAACGACGCCCAGT
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Location/Qualifiers
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AZ583408.1 GI:11703261
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84112, USA
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Matches 1
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AZ583408/c
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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QQ

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymelectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Wector DNA was prepared from a derivative of pWD42 (gill4[DAF12072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli KL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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20 C

BASE COUNT ORIGIN

ô 0; Gaps Query Match
71.1%; Score 12.8; DB 28; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 2; Indels (

3 GGAGGGGGAGGTGGGG 18 g ò

Search completed: October 27, 2003, 13:59:28 Job time: 1582.77 secs

Sequence 1, Appli Sequence 348, App Sequence 22, Appl Sequence 22, Appl Sequence 66, Appl Sequence 101, App Sequence 101, App Sequence 2, Applip

Sequence 265, App Sequence 3, Appli Sequence 3, Appli Sequence 93, Appli Sequence 3, Appli

Sequence Sequence Sequence

Sequence 3, Appli Sequence 117, App Sequence 348, App

us-09-331-204a-8.szlm22.rni

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US-08-229-878-978-9
Sequent No. 593255
Sequent No. 593255
GENERAL INFORMATION OF OBSETIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SECURIORS: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STREET: 3000 S. Augusta Court
CITY: La Habra
STREET: United States of America
COUNTRY: United States of America
STREET: United States of America
COUNTRY: United States of America
STREET: United States of America
COUNTRY: United States of America
STREET: United States of America
COUNTRY: United States of America
STREET: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
MEDIUM TYPE: WordPerfect 6.1
CURRENT APPLICATION NUMBER: 13-SEP-1995
FLING DATE: 13-SEP-1995
CLASSIFICATION NUMBER: 33,880
REGISTRATION:
REGISTRATION: NUMBER: 33,880
REGISTRATION: NUMBER: 13-800
REGISTRATION: NUMBER: 13-800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.4; DB 2;
Pred. No. 1.6e+02;
0; Mismatches 1;
ALIGNMENTS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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94.4%;
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                                       Query Match
Best Local Similarity 94.4
Matches 17; Conservative
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SEQUENCE CHARACTERISTICS
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   nucleic acid
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                                                                                                                                                                                                                                                                                        RESULT 1
US-08-529-878B-3
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192.304 Million cell updates/sec
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Sequence 175
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Sequence 45
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/cgn2_6/ptodata/11/ina/5B_COMB.seq:*
/cgn2_6/ptodata/11/ina/A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-529-878B-44
US-08-529-878B-44
US-09-629-644A-174
US-09-629-674-45
US-09-629-677-45
US-08-248-138-37
US-08-484-138-37
US-08-484-138-37
US-08-484-138-37
US-08-484-138-37
US-08-481-138-37
US-08-491-175
US-09-044-966-72
US-09-044-968-72
US-09-044-968-72
US-09-044-968-72
US-09-644A-175
US-09-646-918-2
US-08-632-575B-19
US-08-632-575B-19
US-08-632-575B-19
US-08-86-913-2
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - nucleic search, using sw model
                                                                                        October 27, 2003, 10:32:34
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Gapop 10.0 , Gapext 1.0
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18
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Perfect score:
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Maximum DB
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Sequence 45, Application US/08529878B

Patent No. 593286

GENERAL INFORMATION:
PAPLICANT: Tam, Nobert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS: 48

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Crockett & Fish STREE: California CITY: La Habra COUNTRY: United States of America STREE: United States of America COUNTRY: United States of America COMPTER: IBM PC COMPATIBLE FORM: MEDIUM TYPE: Floppy disk COMPTER: IBM PC COMPATIBLE FORM: MEDIUM TYPE: WordPerfect 6.1

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/529,878B

FILING DATE: 13-SEP-1995

CLASSIFICATION NUMBER: 213,003

TELECOMMUNICATION NUMBER: 213,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
91.1%; Score 16.4; DB 2;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1;
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                     APPLICATION NUMBER: US/08/529,878B FILING DATE: 13-SEP-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INPORMATION: NAME: Fish, Robert D. REGENGE/DOCKET NUMBER: 213/003 REFERENCE/DOCKET NUMBER: 213/003 TELECOMMUNICATION INFORMATION: TELEPHONE: 714-525-3303 TELEX: 714-525-3303
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
"TYPE: nucleic acid
"TRPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                      INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH. 21 base pairs
TYPE: nucleic accid
STRANDEDNESS: unknown
CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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                                                                                                        SEGUENCE 44, APPLICATION US/OBSZER/RBB
PERGENT NO. 593256
GENERAL INFORMATION:
APPLICANT: Tam. Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Crockett & Fish
STARER: California
STARE: California
STARE: United States of America
COUNTRY: United States of America
ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Toppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION NUMBER: 33,880
REGISTERATION NUMBER: 31,800
REGISTERATION NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELEBRONE: TISH, ROBER D.
TELEBRONE: TISHERDEN: TISHERDE
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Patent No. 593256
GENERAL INFORMATION:
APPLICANT: Tan Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
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STATE: California
COUNTXY: United States of America
ZIP: 90631
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
                         RESULT 2
US-08-529-878B-44
; Sequence 44, Application US/08529878B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 714-525-34:
TELEFAX: 714-525-3303
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STRANDEDNESS:
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US-08-529-878B-4
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Sequence 45, Application US/09092077

Patent No. 6194142

GENERAL INFORMATION:

APPLICANT: Montagnier, Luc

TITLE OF INVENTION: Nucleotide Sequences Derived From The

TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The

TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,

TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis

TITLE OF INVENTION: Of The Diseases Due To Those Viruses

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
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                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.7%; Score 13.8; DB 3;
88.2%; Pred. No. 1.7e+03;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/08/472,928
FILING DATE: 07-UN 1995
APPLICATION NUMBER: US 08/160,465
FILING DATE: 02-DEC-1993
FILING DATE: 20-SEP-1989
FILING DATE: 06-SEP-1989
FILING DATE: 06-SEP-1989
APPLICATION NUMBER: FR 8907354
FILING DATE: 06-SEP-1989
APPLICATION NUMBER: FR 8907354
FILING DATE: 06-SEP-1989
APPLICATION NUMBER: 125,146
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,0062-02000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: ISM PC COMPATIBLE
SOFTWARE: PACENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,077
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Patent No. 5571337
GENERAL INPORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Ren, Wu-Yun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGGAGGGGGAGGTGGGG 18
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-092-077-45
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  US-09-092-077-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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GENERAL INFORMATION:
GENERAL INFORMATION:
Lex M. COWSETT
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
ANTISENSE MODULATION OF PTPIB EXPRESSION
THE REFERENCE:
RTS-0093
CURRENT APPLICATION NUMBER: US/09/487,368A
CURRENT FILING DATE:
240
SEQ ID NO::
LENGTH: 20
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Patent No. 649245

GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Susan M. Freder
APPLICANT: Madeline Wyatt
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Mobert McKay
TITLE OF INVENTION: ANTENSE MODULATION OF PTP1B EXPRESSION
FILE REFERENCE: ISPH-0478

CURRENT REPLICATION NUMBER: US/09/629,644A

CURRENT FILING DATE: 2000-07-31

PRIOR FILING DATE: 2000-07-31

PRIOR FILING DATE: 2000-01-18

WUMBER OF SEQ ID NOS: 242

LENDTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.7%; Score 13.8; DB 3; Length 20; Best Local Similarity 88.2%; Pred. No. 1.7e+03; Matches 15; Conservative 0; Mismatches 2; Indels
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-09-487-368A-174
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                                                                                                                                                                                                                                                                Sequence 174, Application US/09487368A
Patent No. 6261840
                                                                             1 TTGGAGGGGGAGGTGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Watenabe, Kyoichi A.
APPLICANT: Well, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS: 43
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.4%; Score 13.4; DB 5; 93.3%; Pred. No. 2.5e+03; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

74.4%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1;
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ADDRESSEE:

ADDRESSEE:

COOPER T 1185 Avenue of the Americas
CTTY:
New York
STATE: New York
COUNTRY.
IN 0.3.A.
ZIP: 10036
COMPUTER: 18MP
COMPUTER: TEM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06379
FILING DATE: May 13, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
       TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                      TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
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PCT-US95-06379-37
                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-484-138-37
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Best Local Similarity 93.3
Matches 14; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
                                                                                                                                                              LENGTH: 19 base pairs
TYPE: nucleic acid
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US-09-422-978-9409/C
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PCT-US95-06379-37
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Patent No. 5652350
GENERAL INFORMATION:
APPLICANT: Watenabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Ren, Wu-Yun
APPLICANT: Rel, Wu-Yun
APPLICANT: 1185 Avenue of the Americas
STREET: 1185 Avenue of the Americas
TITLE OF INVENTION: Complementary DNA and Toxins NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
CORRESEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 44683-Z/JPW/MJG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
"TING DATE: Unn 7, 1995
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STATE: New York
COMPUTE: New York
COMPUTE: 10.12
COMPUTE: 1.0.12
COMPUTE: 1.0.12
COMPUTE: 1.0.12
COMPUTE: 1.0.144Mb
COMPUTE: 1.0.10
COMPUTE: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 4468.
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: 212-64-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGAGGGGGAGGTGGG 17
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SEQUENCE CHARACTERISTICS:
1.FNGTH: 19 base pairs
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STRANDEDNESS: double
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Best Local Similarity
Matches 14; Conserval
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us-09-331-204a-8.szlm22.rni

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Sequence 26, Application US/09495140

Sequence 26, Application US/09495140

Sequence 26, Application US/09495140

Patent No. 6376182

APPLICANT: CHAO, LIEE

APPLICANT: CHAO, ULLE

APPLICANT: SONG, QING

ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING

ITILE OF INVENTION: DESSENTIAL HYPERTENSION

ITILE OF INVENTION: OF ESSENTIAL HYPERTENSION

ITILE OF INVENTION: OF ESSENTIAL HYPERTENSION

CURRENT APPLICATION NUMBER: US/09/495,140

CURRENT FILING DATE: 2000-01-31

BARLIER APPLICATION NUMBER: 09/889,566

EARLIER APPLICATION NUMBER: 09/886,141

BARLIER FILING DATE: 1999-09-03

BARLIER FILING DATE: 1997-05-14

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-495-140-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
                                                                                                                                                                                                                                                            ANTI-SENSE: no ONIGINAL SOURCE: no ONIGINAL SOURCE: ORGANISM: Homo sapiens PUBLICATION INFORMATION: A M, Orkin, S H. AUTRORS: Michelson, A M, Orkin, S H. TITLE: The 3' untranslated regions TITLE: of the duplicated human alpha-globin genes are TITLE: unexpectedly divergent JOURNAL: Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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; RELEVANT RESIDUES IN SEQ ID NO: 127 :FROM 1 TO 17
US-08-173-489C-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
71.1%; Score 12.8; DB 2;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: alpha-1-globin gene (accession
DESCRIPTION: V00491) nucleotides 827 to 843
HYPOTHETICAL: no
                                                            TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FBATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGAGGGGAGGTGGGG 18
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   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLUME: 22
PAGES: 371-377
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US-08-639-501-72
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LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1...20 TO GOWIST PER AMPLIANTION DE LA POSTA DE SEQ 1544, IN COMPLEMENT US-09-422-978-9409
                                                                        APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density.
TITLE OF INVENTION: Biallelic markers for use in constructing a high density.
TITLE OF INVENTION UNMER: US/09/422,978
CURRENT APPLICATION UNMER: US 09/298,850
EARLIER FILING DATE: 1999-10-20
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.4%; Score 13.4; DB 4; Length 20; Best Local Similarity 93.3%; Pred. No. 2.5e+03; Matches 14; Conservative 0; Mismatches 1; Indels
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| Sequence 127, Application US/08173489C
| Sequence 127, Application US/08173489C
| Patent No. 5861244
| GENERAL INFORMATION:
| APPLICANT: WANG, C. -G.
| APPLICANT: WANG, C. -G.
| TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| NUMBER OF SEQUENCES: 365
| CORRESPONDENCE ADDRESS: 365
| ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET, CITY: NEW YORK
| CITY: NEW YORK
| STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NEW YORK
COUNTRY: USA
ZIP: 10011
ZIP: 10011
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYZEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ 1D NO: 127:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION UNDERF: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Oseph H.
REGISTRATION UNMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
Sequence 9409, Application US/09422978 Patent No. 6537751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo Sapiens
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APPLICANT: Tartigian, Sean V.
APPLICANT: Kamb, Alexander
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Couch, Fergus
APPLICANT: Rommens, Johanna
APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,946
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION NOMBER: 06/039,301
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/056,559
FILING DATE: 21-DEC-1955
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/57,359
FILING DATE: 20-DEC-1955
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/573,779
FILING DATE: 18-DEC-1955
ATTORNEY/ACENT INFORMATION:
NAME: Inhen, Jeffrey L:
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/639,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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Pest Local Similarity 87.5%;
Matches 14; Conservative
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 base pairs
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MOLECULE TYPE: DNA
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0
                                                                                                                                  APPLICANT: Tarti;
APPLICANT: Kamb, Alexander
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Commens, Johanna
APPLICANT: Rommens, Johanna
APPLICANT: Lagure Response R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12.8; DB 2; Length 18; Pred. No. 4.3e+03; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUUTRY: WESTINGSON
STATE: DC
COUNTRY: USA
ZUP: 22204
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
COMPUTER: DE PC compatible
COMPUTER: DE PC compatible
COMPUTER: DAPLICATION DATA:
APPLICATION NUMBER: US 08/685,391
FLING DATE: 12-0APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/585,391
FLING DATE: 11-0AN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FRING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FRING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,359
FRING DATE: 18-DEC-1995
FRING DATE: 18-DEC-1995
FRING DATE: 18-DEC-1995
ATTORNEY AGENT INFORMATION:
NUMBE: INFORMATION:
NUMBER: LANGER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTORNEY AGENT INFORMATION:
NUMBE: INFORMATION:
NUMBE: LANGER: US 08/573,779
FILING DATE: US 08/573,779
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REGISTRATION NUMBER: 28,957
REFERENCET NUMBER: 24884-116802-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
Sequence 72, Application US/08639501
Patent No. 5837492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
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Best Local Similarity 87.5%;
Matches 14; Conservative (
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ORGINAL SOURCE:
CRGANISM: Homo sapiens
US-08-639-501-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                      Patent No. 5837492
GENERAL INFORMATION:
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STRANDEDNESS:
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RESULT 15 US-08-04-946-72 Sequence 72, Application US/09044946 ; Patent No. 6033857

TTGGAGGGGAGGTGG 16

Appl

OM nucleic

Run on:

Seguence:

Searched:

Database

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Sequence 3257, Ap Sequence 1933, Ap Sequence 1937, Ap Sequence 181, App Sequence 1256, App Sequence 1590, Ap Sequence 1566, App Sequence 2556, App Sequence 2570, App
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NESCUL 1.

NESCUL 1.

Sequence 30, Application US/10303109A

Sequence 30, Application US/10303109A

Publication No. U520030194726A1

GENERAL INFORMTION:

APPLICANT: BOLCHAKOVA, Elena

APPLICANT: BOLCHAKOVA, Elena

APPLICANT: ROZZELLE, James

TITLE OF INVENTION: INFERMS OSHIMA! Nucleic Acid Polymerases

FILE REFERENCE: 4777US

CURRENT APPLICATION NUMBER: US/10/303,109A

CURRENT FILING DATE: 2002-11-22

PRIOR FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 39

SOFTWARE PERCENT NESSUL NESSUL 1: 30

NUMBER OF SEQ ID NOS: 39

SOFTWARE PERCENT NESSUL NESSUL 1: 30

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
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                                       1 US-09-382 860-181

1 US-09-382 860-181

1 US-09-936-1256

1 US-09-930-423-1590

2 US-10-061-201-1956

2 US-10-061-201-1956

2 US-10-061-201-1956

2 US-10-084-636A-2570

2 US-10-084-839-2270

2 US-10-084-839-2270

2 US-10-089-893

1 US-09-780-53A-893

1 US-09-745-237A-1591

1 US-09-745-237A-1591

1 US-09-745-237A-1591

2 US-10-205-309-49

1 US-09-948-005-30

2 US-10-205-309-49

1 US-09-948-005-30

2 US-10-205-309-49

1 US-09-948-005-30

1 US-10-205-309-49

1 US-10-024-369-33
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Pred. No. 6.9e+03;
0; Mismatches 1;
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3-09-932-300-10
3-09-932-300-24
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Patent No. US20020055479A1
GENERAL INFORMATION:
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93.8%;
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APPLICANT: Jacqueline Wyatt
APPLICANT: Susan M. Freier
APPLICANT: Brett P. Monia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAGGTGGAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Thermus oshimai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-854-883-174
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Sequence 1936, Ap
Sequence 67, Appl
Sequence 67, Appl
Sequence 28, Appl
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Sequence 174, App
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Sequence 894, App
Sequence 26, Appl
                                                                                                                                                               October 27, 2003, 11:25:34; Search time 387.943 Seconds (without alignments) 124:432 Million cell updates/sec
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Sequence 175, 2
Sequence 32, 3
Sequence 34, 1
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-854-883-174
US-10-061-201-1934
US-10-061-201-1936
US-10-061-201-1936
US-10-008-721-67
US-10-010-920-67
US-10-010-920-67
US-10-08-93A-45
US-10-059-888-26
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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18
1 ttggaggggaggtgggg 18
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 22
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Maximum DB seq
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Madeline M. Butler

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PUBLICATION NO. USZO033166229A1
GENERAL INCORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN I
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-05-23
PRIOR PLING DATE: 2001-05-30
                                                                                                                                                              Sequence 1935, Application US/10061201
Publication No. US20030166229A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GAGGGGGAGGTGGGG 18
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ORGANISM: Homo sapiens
US-10-061-201-1935
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APPLICANT: ROBERT MCKAY
TITLE OF INVENTION: ANTISENSE MODULATION OF PTPIB EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF PTPIB EXPRESSION
FILE REFERENCE: ISPH-0556
CURRENT APPLICATION NUMBER: US 09/629,644
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
SEQ ID NO 174
LENGTH: 20
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93.3%; Pred. No. 1.7e+04;
tive 0; Mismatches 1;
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APPLICANT: Shannon,

APPLICANT: Shannon,

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1

TITLE REPERENCE: PED178

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Antisense Oligonucleotide US-09-854-883-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1934, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
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Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-061-201-1934
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    Length 17;
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Query Match 74.4%; Score 13.4; DB 12; Best Local Similarity 93.3%; Pred. No. 1.7e+04; Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1936, Application US/10061201
PUblication No. US20030166229A1
GENERAL INFORMATION, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PE0178
CURRENT APPLICATION NUMBER: US/10/061, 201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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publication No. US20030157704A1

GENERAL INFORMATION:
APPLICANT: Poole, Jason
APPLICANT: Roninson, Igor
APPLICANT: Roninson, Igor
APPLICANT: Chang, Bey-Dih
ITILE OF INVENTION: ERAGENTS AND METHODS FOR IDENTIFYING AND MODULATING
ITILE OF INVENTION: ERAGENTS AND METHODS FOR IDENTIFYING AND MODULATING
ITILE OF INVENTION: ERAGENTS AND METHODS FOR IDENTIFYING AND MODULATING
CURRENT APPLICATION NUMBER: US/10/233,032A
CURRENT APPLICATION NUMBER: US 09/861,925
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PALENTIN Version 3.0
SEQ ID NO 22
LENGTH: 20
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, OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIIa)
US-10-233-032A-22
                                   , OTHER INFORMATION: Description of Artificial Sequence: Primer ON-DHFR-F1
US-10-008-721-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-28
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                                                                                                         Length 19;
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Pred. No. 1.9e+04;
0; Mismatches 3; Indels
                                                                                                       Query Match 74.4%; Score 13.4; DB 14;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09828034
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ahong, Weidong
APPLICANT: Hong, Zhi
APPLICANT: Horg, Zhi
APPLICANT: Horg, Zhi
APPLICANT: Horg, Zhi
APPLICANT: Ferrari, Err
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US. 60/195,852
PRIOR APPLICATION NUMBER: US. 60/195,852
PRIOR APPLICATION NUMBER: US. 60/195,852
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 83.3%;
Matches 15; Conservative (
                                                                                                                                                                                                      2 TGGAGGGGGAGGTGG 16
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US-09-828-034-28/c
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US-10-233-032A-22
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LENGTH: 21
            FEATURE:
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TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
TITLE OF INVENTION: and methods for using
FILE REPERENCE: 98,723-E3
CURRENT APPLICATION NUMBER: US/10/010,920
CURRENT FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: TNN-Inducible Promoters and Methods for Using
FILE REPERENCE: 98,723-E1
CURRENT APPLICATION NUMBER: US/10/008,721
CURRENT FILING DATE: 2001-12-07
FRICA APPLICATION NUMBER: 60/254,649
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.7e+04;
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PRIOR APPLICATION NUMBER: PCT/US01/00670; PRIOR FILING DATE: 2001-01-30; PRIOR PILING DATE: 2001-01-30; PRIOR PILING DATE: 2001-05-23; PRIOR PILING DATE: 2001-05-23; PRIOR PILING DATE: 2001-10-10; NUMBER OF SEQ ID NOS: 4162; SOFTWARE: Acomica Sequence Listing Engine; SOCITWARE: Acomica Sequence Listing Engine; SEQ ID NO: 1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 67, Application US/10010920
Publication No. US20030027165A1
GENERAL INFORMATION:
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Publication No. US20030082745A1
GENERAL INFORMATION:
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Best Local Similarity 93.3%;
Matches 14; Conservative C
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Best Local Similarity 93.3%;
Matches 14; Conservative (
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                                                                                                                                                                                                                                          TYPE: DNA
CNGANISM: Homo sapiens
US-10-061-201-1936
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US-10-010-920-67
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US-10-008-721-67
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LENGTH: 19
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Sequence 26, Application US/10059877

Sequence 26, Application US/10059877

Sequence 26, Application US/10059877

Sequence 26, Application No. US20030157490A1

GENERAL INFORMATION:
HEAD, LEE

APPLICANT: CHAO, JULE
APPLICANT: CHAO, JULIE
APPLICANT: CHAO, JULIE
APPLICANT: SONG, QING
ITILE OF INVENTION: HERHODS AND COMPOSITIONS FOR CORRELATING
ITILE OF INVENTION: HYPERTENSION
ITILE OF INVENTION NUMBER: US/10/059,877

CURRENT FILING DATE: 2002-01-29

PRIOR FILING DATE: 1209-09-03

PRIOR APPLICATION NUMBER: 09/495,140

PRIOR APPLICATION NUMBER: 09/495,141

PRIOR FILING DATE: 1997-05-14

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/10059888
Publication No. US2030025882A1
GENERAL INFORMATION:
APPLICANT: CHAO, LEE
APPLICANT: CHAO, JULIE
APPLICANT: SONG QING
TITLE OF INVENTION: METHODS AND COWPOSITIONS FOR CORRELATING
TITLE OF INVENTION: HYPERTENSION
FILE REFERENCE: 19113.0081U2
CURRENT APPLICATION WUMBER: US/10/059,888
CURRENT FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490Ale = , OTHER INFORMATION: synthetic construct
US-10-059-877-26
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US-10-059-888-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.1%; Score 12.8; DB 12;
87.5%; Pred. No. 2.9e+04;
tive 0; Mismatches 2;
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PRIOR APPLICATION NUMBER: 09/495,140
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 1999-09-03
PRIOR PILING DATE: 1999-09-03
PRIOR PLICATION NUMBER: 08/886,141
PRIOR APPLICATION NUMBER: 08/856,141
PRIOR APPLICATION NUMBER: 08/856,141
PRIOR PRIOR DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
17 GGAGGGGGAGGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.5
Matches 14; Conservative
                                                                         RESULT 12
US-10-059-877-26
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Sequence 894, Application US/09780533A
Publication No. US2030060611A1
GENERAL INFORMATION
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Lary
APPLICANT: Chowits, Bhrat
APPLICANT: Chowits, Bhrat
APPLICANT: Chowits, Bhrat
APPLICANT: Meaber11, Pete
ITILE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Bossiegen, Jim
APPLICANT: Chowrita, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE OF INVENTION NUMBER: US (00/011)
CURRENT APPLICATION NUMBER: US (00/011)
PRIOR APPLICATION NUMBER: US (0/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.1%; Score 12.8; DB 11; Length 17; 87.5%; Pred. No. 2.9e+04; ive 0; Mismatches 2; Indels
                        Length 20;
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                                                                   Indels
                     Score 13; DB 12; I Pred. No. 2.3e+04; 0; Mismatches 0;
                                                                                                                                                                                                                                              RESULT 10
US-09-780-533A-45/c
Sequence 45, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
     72.2%; Scc.
100.0%; Pre
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Best Local Similarity 87.5
Matches 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
                                                                      Conservative
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CRGANISM: Homo sapiens
US-09-780-533A-894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Homo sapiens
                     Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-780-533A-894/c
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3 GGAGGGGGAGGTGGGG 18

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Gaps

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Length 20; Indels

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OTHER INFORMATION: Description of Artificial Sequence; No. US20030077587Ale = COTHER INFORMATION: synthetic construct
US-09-952-464A-32
                                                                                                                                                                                                                                                 Score 12.8; DB 11;
Pred. No. 2.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: October 27, 2003, 19:00:53 Job time : 387.943 secs
              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jacquelle Wyatt
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Badeline W. Buller
APPLICANT: Madeline M. Buller
APPLICANT: Robert McKay
ITLE OF INVENTION: ANTISENSE MODULATION OF PTPIB EXPRESSION
FILE REFERENCE: ISPH-0576
CURRENT FILING DATE: 2000-05-13
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-07-31
PRIOR PELING DATE: 2000-01-18
PRIOR PELING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR PILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR PILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR PILING DATE: 2000-01-18
   Score 12.8; DB 14; Length 17;
Pred. No. 2.9e+04;
0; Mismatches 2; Indels (
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APPELICANT: Stone, Bawin M.
APPLICANT: Stone, Wallace L.M.
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Finger, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
FILE REFREENCE: 21087 0017011
CURRENT APPLICATION NUMBER: US/09/952,464A
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/461,542
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR PRIOR DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 09/366,952
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR SPLICATION NUMBER: 08/62,999
PRIOR FILING DATE: 1998-04-07
PRIOR SPECIFICATION NUMBER: 08/62,999
PRIOR FILING DATE: 1998-04-07
PRIOR PRIOR DATE: 1998-04-07
PRIOR PRIOR DATE: 1998-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Antisense Oligonucleotide US-09-854-883-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/09952464A Publication No. US20030077587A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 175, Application US/09854883 Patent No. US20020055479A1 GENERAL INFORMATION:
ch 71.1%;
1 Similarity 87.5%;
14; Conservative
                                                                                                                               3 GGAGGGGGAGGTGGGG 18
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ORGANISM: Artificial Sequence
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Query Match
Best Local S:
Matches 14
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(without alignments)
253.343 Million cell updates/sec
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(GGDZ 6/ptodata/1/pna/PCTUS COMB.seq: *
(GGDZ 6/ptodata/1/pna/USO6 COMB.seq: *
(GGDZ 6/ptodata/1/pna/USO8 
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            - nucleic search, using sw model
                                                                                                                                                                                 October 27, 2003, 10:32:35
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Gapop 10.0 , Gapext 1.0
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18
1 ttggaggggaagtac
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Maximum DB seq length: 22
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45 (GHTZ 6/Picolate A/1/Pin/VIGIORD COMB 1864; 466 (GHTZ 6/Picolate A/1/Pin/VIGIORD COMB 1864; 476 (GHTZ 6/Picolate A/1/PinA/VIGIORD COMB 1864; 476 (GHTZ 6/Picolate A/1/PinA/VIGEODO CO
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ednence dhence dhence
ID	18 19 US-09-331-204-5 18 19 US-09-331-204A-8 18 8 US-08-387-041A-3 18 19 US-09-331-204-1
	9 9 9 9
Query Match Length DB	88 88 88 स्टाम्स
	100.0 100.0 91.1
Score	18 18 16.4 16.4
Result No.	H 01 10 4

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18; Conservative

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                                                                                                 Sequence 17, Appl Sequence 42, Appl Sequence 4, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 73, Appl Sequence 17, Appl Sequence 11, Appl Sequence 114, Appl Sequence 174, Appl Sequence 45, Appl Sequence 174, Appl Sequence 45, Appl Sequence 174, Appl Sequence 51847, Appl Seq
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) Sequence 5, Application US/09331204
) GENERAL INFORMATION:
) APPLICANT: Tam, Robert

TITLE OF INVENTION: IMMURE RESPONSE
) TITLE OF INVENTION: IMMURE RESPONSE
) TITLE OF INVENTION IMMURE RESPONSE
) FILE REFERENCE: ICNSequence
) CURRENT APPLICATION NUMBER: US/09/331,204
) CURRENT FILING DATE: 1999-08-20
) PRIOR APPLICATION NUMBER: CI/US97/23927
) PRIOR PILING DATE: 1997-12-19
) NUMBER OF SEQ ID NOS: 6
) SEQ ID NOS: 6
) SEQ ID NOS: 6
) SEQ ID NO 5
) LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Artificial Sequence
CRGANISM: Artificial Sequence
CRGANISM:
CHER INFORMATION: Description of Artificial Sequence: An oligomer
CTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
CTHER INFORMATION: acid. This term includes oligomers consisting of
CTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-5)
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Score 18; DB 19; Length 18; Pred. No. 5.1e+03;

100.0%;

Query Match Best Local Similarity

```
Sequence 8, Application US/09331204A

Sequence 8, Application US/09331204A

GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TILE OF INVENTION:
FILE REFERENCE: 216/01-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT PILING DATE: 1999-08-20
PRIOR PRIOR PRILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 18
LENGTH: 18
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
TITLE OF INVENTION: OF CD28 EXPRESSION
WUMBER OF SEQUENCE: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
ZIP: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,041A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 825.27
REGISTRATION NUMBER: 825.27
REGISTRATION NUMBER: 825.27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
FWATH. 18 base pairs
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100.0%; Score 18; DB 19;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 18; Conservative 0; Mismatches 0;
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18
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; ORGANISM: synthetic construct
US-09-331-204A-8
     1 TTGGAGGGGGAGGTGGGG
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TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                              RESULT 2
US-09-331-204A-8
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US-08-387-041A-3
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APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
US/09/31,204A
CURRENT APPLICATION NUMBER: US/09/331,204A
FILE REPRENCE:
CURRENT APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID ADTS: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
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APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
FILE REPERENCE: Cl041/7010 (AMS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
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APPLICANT: Injeford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonuclectides and Uses
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91.1%; Score 16.4; DB 19;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1;
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FastSEQ for Windows Version 3.0
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1999-09-03
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                                                                                                             ; Sequence 7, Application US/09331204A ; GENERAL INFORMATION:
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    1 TTGGAGGGGGTGGTGGGG 18
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ORGANISM: Artificial Sequence
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Best Local Similarity 94.4
Matches 17; Conservative
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PRIOR FILING DATE: 1999-0:
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Win
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                                                                                            US-09-331-204A-7
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LENGTH: 18
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APPLICANT: Tam, Robert
TICN PLANTION: Tam, Robert
FILE OF INVENTION: 216/013-031
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT APPLICATION NUMBER: DS/09/331,204A
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1999-08-10
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TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION WINBER: US)-99331,204
CURRENT FILING DATE: 199-08-20
PRIOR APPLICATION NUMBER: DCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: An oligomer OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic OTHER INFORMATION: acid including oligomers consisting of naturally OTHER INFORMATION: occurring bases, sugars and intersugar US-09-331-204-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 2.1e+04;
0; Mismatches 1;
                                                                                        Score 16.4; DB 8;
Pred. No. 2.1e+04;
0; Mismatches 1;
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GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 18
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TOPOLOGY: unknown
NLECULE TYPE: DNA (genomic)
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, ORGANISM: synthetic construct
US-09-331-204A-4
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                     Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity
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US-08-387-041A-3
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LENGTH: 18
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RESULT 12
US-09-331-204A-6
; Sequence 6, Application US/09331204A
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Matches 17; Conserv
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GENERAL INFORMATION:
APPLICANT: Tam. Robert
TITLE OF INVENTION: IMMUNE RESPONSE
TITLE OF INVENTION: IMMUNE RESPONSE
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR FILING DATE: 1999-08-20
PRIOR SPPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 19
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CTHER INFORMATION: Description of Artificial Sequence: An oligomer;
CTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
CTHER INFORMATION: acid. This term includes oligomers consisting of
CTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-4)
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
TITLE OF INVENTION: OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 41
CORRESPONDENCES: 4
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 91.1%; Score 16.4; DB 19; Length 19; Similarity 94.4%; Pred. No. 2.1e+04; 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                        Length 18;
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Pred. No. 2.1e+04;
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91.1%; Score 16.4; D
Best Local Similarity 94.4%; Pred. No. 2.1e
Matches 17; Conservative 0; Mismatches
TITLE OF INVENTION: Thereof
FILE REFERENCE: C1041/7010 (AWS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/FEP99/06502
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 17; Conserv
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STATE: Ne
COUNTRY:
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US-08-387-041A-4
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LENGTH: 18
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US-09-31-204-6
| Sequence 6, Application US/09331204
| GENERAL INFORMATION: APPLICANT: Tam, Robert
| TITLE OF INVENTION: MANUE RESPONSE |
| TITLE OF INVENTION: MANUE RESPONSE |
| FILE REPRENCE: ICNSequence |
| CURRENT APPLICATION NUMBER: US/09/331,204 |
| CURRENT FILING DATE: 1999-08-20 |
| PRIOR PILING DATE: 1997-12-19 |
| NUMBER OF SEQ ID NOS: 6 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 6 |
| LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.1%; Score 16.4; DB 8; Length 21; 94.4%; Pred. No. 2.1e+04; Live 0; Mismatches 1; Indels
COMPUTER READABLE FORM:

MEDLUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEACHIN Release #1.0, Version #1.30
SOFTWARE: Pacentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,041A
FILING DATE: 02-FEB.1995
CLASSIFICATION: 5.14
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 3560
TELEPHONE: 415-854-3660
TELEPHONE: 415-854-3664
TELEPHONE: 415-854-3664
TELEPHONE: 415-854-3664
TELEPHONE: 25,227
TELEPHONE: 415-854-3664
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Gaps

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RESULT 15
US-09-979-666B-79
Sequence 79, Application US/09979666B
GENERAL INFORMATION:
APPLICANT: TACHAS, GENERE
TITLE OF INVENTION: INHIBITION OF GASTRIC ACID PRODUCTION AND/OR SECRETION
FILE REFERENCE: 47-162
CURRENT APPLICATION NUMBER: US/09/979,666B
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin Ver. 2.1
LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
OTHER INFORMATION: Synthetic antisense oligonuclectide, can be of OTHER INFORMATION: RNA, DNA or chimera
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Syntheti
OTHER INFORMATION: antisense oligonuclectide, can be RNA, DNA
US-09-979-6668-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%; Score 14.8; DB 42; Length 22; 81.2%; Pred. No. 8.3e+04; cive 3; Mismatches 0; Indels (
            Indels
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0
         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TGGAGGGGGAGGTGGG 17
                                                                                                3 GGAGGGGGAGGTGGG 17
                                                      3 GGAGGGGGAGGTGGG 17
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Best Local Similarity 81.2
Matches 13; Conservative
         15; Conservative
         Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSECTEGEMENTICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 47426
GENERAL INFORMATION:
APPLICANT: TON Pharmaceuticals, Inc.
APPLICANT: Tan, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respondence: 216/013-012.
FILE REPERENCE: 216/013-013.
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR PILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
LENGTH: 21
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSELESCENCICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION UNMBER: US/10/310,188
CURRENT APPLICATION UNMBER: US/10/310,188
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 38927
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 19; Length 21; 2.1e+04; hes 1; Indels
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Best Local Similarity 94.1%; Pred. No. 4.9e+04;
Matches 16; Conservative 0; Mismatches 1; Indels
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100.0%; Pred. No. 6.9e+04;
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Pred. No. 2.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: synthetic construct
US-09-331-204A-6
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-310-188-38927
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US-10-310-188-38927
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Gaps

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Sequence 39102, Sequence 41647, Sequence 58279, Sequence 610182, Sequence 61011, Sequence 10781, Sequence 38912, Sequence 18827, Sequence 1882
                                                                                                             51842,
58279,
60182,
61077,
72811,
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PCT-USO2-38216-39031
PCT-USO2-38216-39102
PCT-USO2-38216-51842
PCT-USO2-38216-51842
PCT-USO2-38216-6107
PCT-USO2-38216-6107
PCT-USO2-38216-6107
PCT-USO2-38216-6107
PCT-USO2-38216-10778
PCT-USO2-38216-10778
PCT-USO2-38216-18422
PCT-USO2-38216-18422
PCT-USO2-38216-18227
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                                                                                                                                                                                                                                                                              October 27, 2003, 11:09:34 ; Search time 307.029 Seconds (without alignments) 97.777 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pending Patents_NA_New:*

/ cgn2_6/ptodate1/l/pna/PCT_NEW_COMB.seq:*

/ cgn2_6/ptodata1/l/pna/US07_NEW_COMB.seq:*

/ cgn2_6/ptodata1/l/pna/US07_NEW_COMB.seq:*

/ cgn2_6/ptodata1/l/pna/US07_NEW_COMB.seq:*

/ cgn2_6/ptodata1/l/pna/US09_NEW_COMB.seq:*

/ cgn2_6/ptodata1/l/pna/US09_NEW_COMB.seq:*

/ cgn2_6/ptodata1/l/pna/US10_NEW_COMB.seq:*

/ cgn2_6/ptodata1/l/pna/US60_NEW_COMB.seq:*
                                              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2231628 segs, 833900706 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                          nucleic search, using sw model
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18
1 ttggagggaggtgggg 18
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Gapop 10.0 , Gapext 1.0
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Query
Match Length D
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Perfect score:
Sequence:
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RESULT 1
PCT-USO2-38216-47426

SQUIGNEG 47426, Application PC/TUSO238216

SQUIGNEG 47426, Application PC/TUSO238216

SQUIGNEG 47426, Application PC/TUSO238216

SQUIGNEG 47426, Application PC/TUSO238216

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT RELING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Parentin version 3.2

SEQ ID NO 47426

LENGTH: 19

TYPE: DAA

COGRANISM: Homo sapiens

PCT-USO2-38216-47426 RESULT 2
PCT-USO2-38216-38927
FCT-USO2-38216-38927
GENERAL INFORMATION:
JENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY;
TITLE OF INVENTION: GENER AND USES THEREOF;
TITLE OF INVENTION: GENER AND USES THEREOF;
TITLE OF INVENTION: GENER AND USES THEREOF;
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 38927
LENGTH: 18
TYPE: DAA
CREAN: Homo sapiens
PCT-USO2-38216-38927 ö ö Gaps ô ö Ouery Match

Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels Query Match
Best Local Similarity 94.1%; Pred. No. 5.9e+03;
Matches 16; Conservative 0; Mismatches 1; 2 TGGAGGGGGAGGTGGGG 18

Sequence 47426, A Sequence 1866, Ap Sequence 17706, Ap Sequence 26611, A Sequence 1741, App Sequence 18129, A Sequence 18169, A Sequence 1816, A Sequence 1829, A Sequence 1816, A Sequence 1818, Ap Sequence

PCT US02 - 38216 - 47426
PCT US03 - 26780 - 1166
PCT US03 - 26780 - 1166
PCT US03 - 26780 - 1166
PCT US02 - 38216 - 47706
PCT US02 - 38216 - 26651
US-09-629 - 6444-174
PCT US02 - 38216 - 6227
PCT US02 - 38216 - 5897
PCT US02 - 38216 - 51829
PCT US02 - 38216 - 64492
PCT US02 - 38216 - 64492
PCT US02 - 38216 - 64492
PCT US02 - 38216 - 1829
PCT US02 - 38216 - 1829
PCT US02 - 38216 - 1836
PCT US02 - 38216 - 1829
PCT US02 - 38216 - 1836
PCT US02 - 38216 - 18829
PCT US02 - 38216 - 18829
PCT US02 - 38216 - 18816

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RESULT 5
PCT-1902-38216-26651/c
Sequence 26651, Application PC/TUS0238216
Sequence 26651, Application PC/TUS0238216
Sequence 26651, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: ROSELta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION UNDER: PCT/US02/38216
CURRENT PALLICATION NUMBER: PCT/US02/38216
CURRENT PALLICATION NUMBER: PCT/US02/38216
CURRENT PLING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 26651
LENGTH: 19
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US-09-629-644A-174

US-09-629-644A-174

Sequence 174, Application US/09629644A

GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Robert D. Monia
APPLICANT: Robert Madeline M. Butler
APPLICANT: Robert McRay
TILE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
FILE REFERENCE: ISPH-0478
CURRENT FILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 242

SEQ ID NO 174
LENGTH: 20
LENGTH: 20
LENGTH: 20
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Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.7%; Score 13.8; DB 1; Length 19; Best Local Similarity 88.2%; Pred. No. 2.2e+04; Matches 15; Conservative 0; Mismatches 2; Indels
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, OTHER INFORMATION: Antisense Oligonucleotide
US-09-629-644A-174
      Mismatches
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PCT-US02-38216-51847
; Sequence 51847, Application PC/TUS0238216
; GRNEAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
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                                                                       3 GGAGGGGGAGGTGGGG 18
          15; Conservative
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ORGANISM: Homo sapiens
PCT-US02-38216-26651
             Matches
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GENERAL INFORMATION: HOWER THERAPDUTICS, INC.
APPLICANT: FUTER MET THERAPDUTICS, INC.
TITLE OF INVENTION: HUMAN POLYEPPITIES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE PRICES.
FILE REPERENCE: 08940.0014.00304
CURRENT APPLICATION WARER: PCT/USGS/26780
CURRENT APPLICATION WARER: 06/406.516
PRIOR FILING DATE: 2002-08-29
PRIOR PRIOR APPLICATION WARER: 60/406,56
PRIOR APPLICATION WARER: 60/406,56
PRIOR APPLICATION WARER: 60/406,66
PRIOR APPLICATION WARER: 60/406,66
PRIOR APPLICATION WARER: 60/406,66
PRIOR PLING DATE: 2002-08-29
PRIOR PLING DATE: 2002-08-29
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PRIOR PRIOR PLING DATE: 2002-08-29
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PRIOR PLING DATE: 2002-0
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PCT-1062-38216-47706
Sequence 47706, Application PC/TUS0238216
Sequence 47706, Application PC/TUS0238216
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT PLING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSEQ ID NO 47706
LENGTH: 22
LENGTH: 22
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             3 GGAGGGGGAGGTGGG 17
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CRGANISM: Homo sapiens
PCT-US02-38216-47706
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Best Local Similarity
Matches 15; Conservi
                                                                                                                                                                         RESULT 3
PCT-US03-26780-1166
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Score 14.4; DB 1; Length 22; Pred. No. 1.3e+04;

80.0%; 93.8%;

Query Match Best Local Similarity

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RESULT 10
PCT-USO2-18216-18977
SEQUENCE 38977, Application PC/TUSO238216
SEQUENCE 38977, Application PC/TUSO238216
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
CURRENT PELING DATE: 2002-11-12
CURRENT PILING DATE: 2002-11-12
SOUTHWARE: PATENTING VARIENCE SEGAL
SOUTHWARE: PATENTING VARIENCE SEGAL
SEG ID NO 38977
TWORTH: 18
TWORTH: 18
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PCT-USO2-38216-36515
Sequence 36515, Application PC/TUSO238216
Sequence 36515, Application PC/TUSO238216
Sequence 36515, Application PC/TUSO238216
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION UNMERS. PCT/USO2/38216
CURRENT PELICAL ODATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE PATENTION OF SECOND OF NOTE OF SECOND OF SECOND OF NOVEL VIRAL REGULATORY
SEQ ID NOS: 86841
SEQ ID NO 36515
LENGTH: 20
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Pred, No. 3e+04;
0; Mismatches 1;
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Best Local Similarity 93.3%;
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
  18 GGTGGGGGAGGTGGG
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CORGANISM: Homo sapiens
PCT-US02-38216-51829
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PCT-US02-38216-51829
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APPLICANT: Rosetta Genomics LTD
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BEING MAND USES THEREOF
FILE REPERENCE: 55002 MAND USES THEREOF
FILE REPERENCE: 55002 MAND TO STATE OF THE REPERENCE: 5002 MANDER: PCT/US02/38216
CURRENT APPLICATION MANDER: PCT/US02/38216
UNMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 25860
LENGTH: 18
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| Sequence 6227, Application PC/TUS0238216
| Sequence 6227, Application PC/TUS0238216
| GENERAL INFORMATION:
| APPLICANT: ROSetta Genomics LTD
| TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
| TITLE OF INVENTION: GENES AND USES THEREOF
| FILLE PEFERENCE: 55002
| CURRENT APPLICATION NUMBER: PCT/US02/38216
| CURRENT PILLING DATE: 2002-11-12
| NUMBER OF SEQ ID NOS: 86841
| SOFTWARE: Patentin version 3.2
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY TITLE OF INVENTION: GENES AND USES THEREOF FILE REPREBNCE: 55002
CURRENT APPLICATION: OWNER: PCT/USO2/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSOTWARER: Patentin version 3.2
SEQ ID NO 51847
LENGH: 21
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Pred. No. 2.2e+04;
0; Mismatches 2; Indels
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; Sequence 25860, Application PC/TUS0238216
; GENERAL INFORMATION:
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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ORGANISM: Homo sapiens
PCT-US02-38216-25860
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CORGANISM: Homo sapiens
PCT-US02-38216-51847
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Best Local Similarity
Matches 14; Conserv
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LENGTH: 18
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Query Match 72.2%; Score 13; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 4.2e+04; Matches 13; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12,
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 64492
LENGTH: 19
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CORGANISM: Homo sapiens
PCT-US02-38216-64492
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SEQUENCE 25810, Application PC/TUSO238216

GENERAL INFORMATION

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REPERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/USO2/38216

CURRENT APPLICATION NUMBER: PCT/USO2/38216

SOFFWARE OF SEQ ID NOS: 86841

SOFFWARE PAPENCH: PAPENCH: SO02-11-12

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PCT-USO2-38216-64492/c
; Sequence 64492, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: ROSELTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECT-USO2-38216-18159, Application PC/TUSO238216
; SEQUENCE 18159, Application PC/TUSO238216
; GENERAL INFORMATION:
    TILLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY;
    TILLE OF INVENTION: GENES AND USES THEREOF
; TILLE REPERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/USO2/38216
; CURRENT PELING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SEQ ID NO 18159
; SEQ ID NO 18159
; LENGTH: 22
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                                                                                                   Query Match 73.3%; Score 13.2; DB 1; Length 20; Best Local Similarity 83.3%; Pred. No. 3.6e+04; Matches 15; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 100.
Matches 13; Conservative
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ORGANISM: Homo sapiens
PCT-US02-38216-18159
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CORGANISM: Homo sapiens
PCT-US02-38216-25810
                  PCT-US02-38216-36515
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Unclassified.
I (bases 1 to 17)
Rando, R.F., Ojwaug, J.O., Hogan, M.E., Wallace, T.L. and Cossum, P.A.
Anti-viral guanosine-rich tetrad forming oligonucleotides
Patent: US 6288042-A 62 11-SEP-2001;
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Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
Anti-viral guanosine-rich tetrad forming oligonucleotides
Patent: US 6288042-A 64 11-SEP-2001;
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Sequence 65 from patent US 6288042,
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Sequence 62 from patent US 6288042.
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G-motif oligonucleotides and uses thereof
Patent: WO 0014217-A 42 16-MRA-2000,
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
Location/Qualifiers
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Viral hemorrhagic septicemia virus
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Rhabdoviridae; Novirhabdovirus.
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Sequence 42 from Patent WO0014217.
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1 (bases 1 to 17)

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Rando, R.F., Fennewald, S., Zendegui, J.G., Ojwang, J.O. and Hogan, M.E. Anti-viral guanosine-rich oligonucleotides and method of treating
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Rando.R.F., Fennewald, S., Zendegui, J.G., Ojwang, J.O., Hogan, M.E., Pommer, Y. and Mazumder, A.
Guanosine-rich oligomucleotide integrase inhibitors
Patent: US 6355785-A 65 12-MAR-2002,
Location/Qualifiers
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Sequence 62 from patent US 6323185.
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Sequence 65 from patent US 6355785.
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1 (bases 1 to 17)
2 Asndo,R.F.F. Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E., Pommier,Y. and Mazumder,A.
Guanosine-rich oligonuclectide integrase inhibitors
Patent: US 6355785.A 62 12-MAR-2002;
Patent: US 6355785.A 62 12-MAR-2002;
                                                                      1 (bases 1 to 17)
Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
Anti-viral guanosine-rich tetrad forming oligonucleotides
Patent: US 6288042-A 65 11-SEP-2001;
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Sequence 64 from patent US 6355785.
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1 (bases 1 to 20)
Acton, S.Laurene
Intronic and polymorphic SR-BI nucleic acids and uses therefor
Patent: US 5998141-A 56 07-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triple-helix forming oligonucleotides for targeted mutagenesis Patent: US 5962426-A 2 05-OCT-1999;
Location/Qualifiers
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                                                      /organism="synthetic construct"
/mol_type="genomic DNA"
/db xxef="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz:Polydesoxyribonuklectid"
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Patent: WO 0179487-A 36 25-OCT-2001;
Degitz, Klaus Karl (DE); Besch, Robert (DE)
Location/Qualifiers
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Sequence 2 from patent US 5962426.
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Glazer, P.M.
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1 (bases 1 to 17)
Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O. and Hogan,M.E.
Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
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I bases 1 to 17)
Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O. and Hogan,M.E.
Anti-viral guanosine-rich oligonucleotides and method of treating
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Location/Qualifiers
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/organism="unknown"
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Location/Qualifiers
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            AR262438 17 bp
Sequence 64 from patent US 6323185.
AR262438 1 GI:28073869
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Sequence 65 from patent US 6323185.
AR266439 1 GI:28073870
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Sequence 36 from Patent WO0179487.
AX284071 1 GI:17044781
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Search completed: October 27, 2003, 11:09:28 Job time : 251.743 secs

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Triplex forming of CD28 inhibiting ph CD28 inhibiting ph Human ETFB allele-Oligonuclectide SE Oligonuclectide HS Oligonuclectide HS Oligonuclectide HS Oligonuclectide HS Oligonuclectide HS ICAM-1 triple hell Transcriptional ac Sequence of B-133-sequence o
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ABF47470
ABF47471
ABH53376
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AAX79259
AAX79263
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16-APR-1997 (first entry)
   WO9624380-A1.
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18-SEP-1995;
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                        The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                                                            Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD28, inhibition, antisense oligonucleotide, interleukin 2, IL-2, immune system mediated disease, gamma-interferon, IL-8;
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                                                                                                                                                                                                                                                                          Length 12;
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                                                                                                                                                                                                                                                                       100.0%; Score 12; DB 17; Length 1 100.0%; Pred. No. 1e+04; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD28 inhibiting phosphorothioate oligonucleotide RT18S.
                                                                                                                                                                                                                      in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                     Sequence 12 BP; 0 A; 0 C; 10 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system-mediated
E CD28, IL-2, gamma-inte
                                                                                                      Example 2; Page 45; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Column 24; 45pp; English.
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                                                                                                                                                                                                                                                                                              12; Conservative
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 (ICNC ) ICN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphorothioate; ss
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                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAMR/) TAM R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                             AAX90341;
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                      ram RC
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The invention comprises DNA, cDNA and protein sequences of the human electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on chromosome 19q13.3-13.4). The invention specifically relates to the identification of 27 novel polymorphic sites within the ETFB gene (located on identification of 27 novel polymorphic sites within the ETFB gene.

Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor circumpary flavoprotein dehydrogenases and is located in the mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta mitochondrial respiratory chain by ETF are transferred to the mitochondrial respiratory chain by ETF are transferred to the mitochondrial respiratory chain by ETF are transferred to the factory of ETFB is a pharmaceutically-important gene in the treatment of Therefore ETFB polymorphisms identified in the invention are useful for genotyping and haplotyping the ETFB gene of an individual. The ETFB protein and function of ETFB in vivo. The ETFB protein and nucleic acids of the invention are useful for studying the expression and function of ETFB in vivo. The ETFB protein and nucleic acids are also useful for testing the efficacy of therapeutic agents and
AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human electron-transfer-flavoprotein, beta polynucleotide, useful for therapeutic purposes, for studying the expression and function of the polynucleotide, and for expressing the flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            electron acceptor; mitochondrial matrix; glutaric acidaemia type II; novel polymorphic site; novel polymorphism; ETFB genotype, ss; GAII; ETFB haplotype, transgenic animal; primer; probe; chromosome 19413; primer-extension oligomuclectide; single nuclectide polymorphism;
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                                                                                                                                                                                                                                                                                                                                                      Length 12;
                                                                                                                                                                                                                                                                                                   100.0%; Score 12; DB 20; Length 1 100.0%; Pred. No. 1e+04; Minatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ETFB allele-specific oligonucleotide primer 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m
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                                                                                                                                                                                                                                                              Sequence 12 BP; 0 A; 0 C; 10 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽₽.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2000; 2000US-215984P.
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Best Local Similarity 100.
Matches 12; Conservative
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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonuclectide (OGN). AAX9028 to AAX9029: represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonuclectide used in the exemplification of the
                                                                                                                                                                                                                                                                                                     CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                Length 18
                                                                                                                                                                                                                                                                                   CD28 inhibiting phosphorothioate oligonucleotide RT03S
               100.0%; Score 12; DB 17;
100.0%; Pred. No. 9.9e+03;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0;
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             Query Match
Best Local Similarity 100.
Matches 12; Conservative
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AAX90332/
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compounds for glutaric acidaemia type II. The nucleic acids of the invention are useful in the production of a transgenic animal expressing the BTFB gene. Nucleic acids ABL39414-ABL39441-ABL39494 represent claimed ETFB allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed ETFB allele-specific PRR primers. Nucleic acids ABL39495 represent claimed ETFB primer-extension pligonucleotides.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reduction, T cell, CD28, gene expression, treatment, immune system, disorder, graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, 5'-UTR, systemic lupus erythematosus, inflammatory bowel disease, triplex forming, oligonucleotide, 5'-untranslated region, ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present oligomuclectide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, soriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                       / Match 100.0%; Score 12; DB 24; Length 15; Local Similarity 100.0%; Pred. No. 1e+04; Nes 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
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                                                                                                            Sequence 15 BP; 0 A; 0 C; 11 G; 3 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 54; 77pp; English.
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95US-0529878.
95US-0387041.
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(first entry)
                                                                                                                                                                                                        1 GGGGTGGTGGGG 12
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18-SEP-1995;
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15-APR-1997
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                                                                                                                                          Query Match
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Matches
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Length 18;

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Length 18;

Synthetic.

Tam RC;

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. AAX90292 to AAX90323 represent oligonucleotides used in the exemplification of the present invention.
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AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD28, inhibition, antisense oligonucleotide, interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
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                                                   Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8 \,
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100.0%; Score 12; DB 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                Example, Column 13; 45pp; English.
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Matches 12; Conservative
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              WPI; 1999-443609/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for inhibiting the expression of CD28, IL-2. gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN) AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                      IL-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                    CD28; inhibition; antisense oligonucleotide; interleukin 2; immune system mediated disease; gamma-interferon; {\rm IL}^- \theta_1 phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide RTC06 used in an Example from US5932556.
CD28 inhibiting phosphorothioate oligonucleotide RTC06S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 12; DB 20; 3
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example, Column 21; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0529878
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ID AAX90297 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGTGGTGGGG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGTGGTGGGG 7
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-443609/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAMR/) TAM R
                                                                                                                                                                                                                                                                                                                    (TAMR/) TAM R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8-SEP-1995;
                                                                                                                                                                                                                                       18-SEP-1995;
                                                                                                                                                                                                                                                                                18-SEP-1995;
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                                                                                                                                                         JS5932556-A
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Gaps

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Length 18;

Synthetic

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AAX90297;

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The present sequence represents a G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides. The G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflections, parasitic infections (e.g. Leishmanissis or Toxoplasmosis), viral infections, parasitic infections (e.g. Leishmanissis or Toxoplasmosis), viral infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage
                                                                                                                                                                                                                                                                                      G-motif oligonucleotide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation, natural killer cell; septic shock; cytocoxic T-lymphocyte, inflammation, autoimmune disease; rhenmatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawaaaki syndrome, graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptrococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
                                                                                                                                                                                                                                                       Nucleotide sequence of G-motif oligonucleotide GR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 14; Page 32; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heeg K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-EP06502
                                                                                                                                   AAZ99625 standard; DNA; 18
                                                                                                                                                                                                                 12-JUL-2000 (first entry)
17
                                   7 GGGGTGGTGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagner H, Lipford GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-256970/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200014217-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                             AAZ99625;
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G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection; antigen presenting cell activation; natural Killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; arcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; baccerial infection; parasitic infection; Lumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                                                                                                                                     Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 14; Page 32; 75pp; English.
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                                                                               AAZ99650 standard; DNA; 18
                                                                                                                               (first entry)
1 GGGGTGGTGGGG 12
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                     GGGTGGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-256970/22.
                                                                                                                                                                                                                                                                                                                                       WO200014217-A2.
                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1998;
                                                                                                                               12-JUL-2000
                                                                                                                                                                                                                                                                                                                                                              6-MAR-2000
                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wagner H,
                                                                                                       AAZ99650;
                                                                  AAZ99650,
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The present sequence represents a non-G-motif oligonuclectide of the invention. The specification describes compositions comprising G-motif clarention. The specification describes compositions comprising G-motif oligonuclectides inhibit activation of antiquen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytoctoxic consistencies for treating septic shock, inflammation, productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell response 1-mediated classases (e.g. Streptococcal induced arthritis, Lume arthritis, chronic inflammatory bowel disease, psortasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections), spontaneous abortions and tumours. They may also be conserved.

Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

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Gaps
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0
100.0%; Score 12; DB 21; Length 18; larity 100.0%; Pred. No. 9.9e+03; Conservative 0; Mismatches 0; Indels
       Query Match
Best Local Similarity
Matches 12; Conserv
                          Best Loca
Matches
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Gaps

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Indels

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Mismatches

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Similarity

Query Match Best Local Simi Matches 12;

100.0%; Score 12; DB 21; Length 18; 100.0%; Pred. No. 9.9e+03;

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2; IL-2;

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).

AAX90288 to AAX90291 represent specifically claimed GGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothiogen oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD28, inhibition, antisense oligonucleotide, interleukin 2, IL-2, immune system mediated disease, gamma-interferon, IL-8, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                        CD28, inhibition, antisense oligonucleotide, interleukin
immune system mediated disease; gamma-interferon; IL-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                         CD28 inhibiting phosphorothioate oligonucleotide RT04S.
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100.0%; Pred. No. 9.8e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD28 inhibition oligonucleotide RT04.
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ВЪ.
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AAX90329 standard; DNA; 21
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                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGTGGTGGGG 12
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                                                                                                                                                                                   phosphorothioate; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-443609/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.
                                                                                                                                                                                                                                                                                                                                                                                                      (TAMR/) TAM R
                                                                                                                                                                                                                                                                                                                                18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1995;
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                                                                        24-SEP-1999
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                                                                                                                                                                                                                                                          US5932556-A
                                                                                                                                                                                                                       Synthetic.
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                                   AAX90329;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tam RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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                                                                                                                                                                                                                                                                                                           Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; sporiasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR; systemic lupus erythematcosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveritis, remumatorid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                         Priplex forming oligo targetting CD28 5'-UTR (nt 58-78).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
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                                                                                                                                              BP.
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95US-0529878.
95US-0387041.
95US-0529878.
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                                                                                                                                              AAT36197 standard; DNA; 21
                                                                                                                                                                                                                     (updated)
(first entry)
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                   1 GGGGTGGTGGGG 12
                                                    12 deserrecredes 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ICNC ) ICN PHARM INC.
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18-SEP-1995;
09-FEB-1995;
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                                                                                                                                                                                                                     25-MAR-2003
15-APR-1997
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Synthetic.

AAT36197;

RESULT 11 AAT3619

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Gaps

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95US-0529878.

18-SEP-1995;

Query Match Best Local S

Matches

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10

RESULT 12 AAX90329

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chromosome 19413.3-13.4). The invention specifically relates to the identification of 27 movel polymorphic sites within the ETPB gene.

C identification of 27 movel polymorphic sites within the ETPB gene.

C Electron-transfer flavoprotein (ETFP) is an obligatory electron acceptor mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta composed of an alpha (ETFA) and a beta (ETFB) subunit. Electrons accepted by ETF are transferred to the mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).

C EFIGIENCY of ETF or ETFDH leads to glutaric acidaemia type II (GAII).

C Therefore ETFB polymorphisms identified in the invention are useful C or genoryphign and haphoryphing the ETFB gene of an individual. The ETFB protein and mucleic acids of the invention are useful for testing the ETFB protein and function of ETFB in vivo. The ETFB protein and nucleic acids of the invention are useful for testing the efficacy of therapeutic agents and compounds for glutaric acidaemia type II. The nucleic acids of the invention are useful in the production of a transgenic animal expressing the ETFB gene of a blanch of the invention are useful in the production of a transgenic acids of the invention are useful in the production of a transgenic acids of the invention are useful in the production of a transgenic acids of the invention are useful in the production of a transgenic acids of the invention are useful in the production of a transgenic acids of the invention are useful in the production of a transgenic acids of the compounds ETFB allele-specific PCR primers. Nucleic acids ABL39494 represent claimed ETFB primer-extension oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 283457 for detecting SNP TSC0011318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11.6; DB 24;
Pred. No. 1.5e+04;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 3 A; 10 C; 1 G; 0 U; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.5e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.78;
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ABH83464 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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O
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                                                                                                                                                                                                                       immune system-mediated diseases by inhibiting E CD28, IL-2, gamma-interferon or IL-8
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                                                                                                                                                                                                                                                                                           Claim 6; Column 29; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL39458 standard; DNA; 15 BP.
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                                95US-0529878
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                                18-SEP-1995;
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ID ABL3
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the human

The invention comprises DNA, cDNA and protein sequences of

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us-09-331-204a-13.szlm22.rng

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The cligomers are also used detecting cell type differentiation. ABC00010-ABE09999, ABF00010-ABF99999, ABH00010-ABF99999 and ABF00010-ABF899999 ABH00010-ABF99999 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of the printed ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                           Query Match

91.7%; Score 11; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   Sequence 12 BP; 2 A; 10 C; 0 G; 0 U; 0 other;
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1 GGGGTGGTGGG 11 11 dederrecrede 1 g

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Gaps

Search completed: October 27, 2003, 11:25:21 Job time : 108 secs

nucleic

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Run δ

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twilc02.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2259362 3' similar to TR:000599 CON1.;, mRNA sequence. AI590540 AI590540.1 GI:4599588
A2447936 IM0245018
A2786591 200018809
A2786592 2000181817
A245588 IM0276J16
A245588 IM0276J16
A274703 200004G14
A118338 G44112.x
A149277 L154602.x
A276671 IM0570018
A2769521 IM0570018
A2769521 IM0570018
A276954 C0190003.x
A2769432 Q417002.x
A156944 C028410.x
A156944 C028410.x
A156954 C0108811.x
A156954 C0108811.x
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A256954 C0108811.x
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B059500 E012790
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Email: cgapbs-r@mail nih.gov

Tissue Producement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

10 Cases 1 to 16.

NOT/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Stockes and Stroke, Brain Tumor Genome Anatomy Project Unpublished.
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                                                                                                    AZ766712

AAZ766712

AAZ769521

AAZ78820

AAZ78820

AAZ88820

AAZ88820

AAZ88852

AAZ88852

AAZ88852

AAZ788520

AAZ7885973

AAZ7885973

AAZ788597

AAZ789590

AAZ8859001

AAZ8959001

AAZ8959001
  EST.
Homo sapiens (human)
Homo sapiens
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  44444444444
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AI590540/c
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DEFINITION
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KEYWORDS
SOURCE
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AIS07936 wf52e09.x
AZ369361 1M0119123
AZ381798 1M0138G01
                                                                                       ; Search time 1054.51 Seconds (without alignments) 276.576 Million cell updates/sec
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Compugen Ltd.
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             GenCore version
Copyright (c) 1993 - 2003
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45 summaries
                                                                nucleic search, using sw model
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AI807936
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                                                                                        October 27, 2003, 10:32:29
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Gapop 10.0 , Gapext 1.0
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Match Length
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Minimum DB Maximum DB

Database

Result 80.

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Searched:

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19 bp DNA linear GSS 02-OCT-2000 close 10kb plasmid UUGCIM library Mus musculus genomic A2369361. A2369361. GI:10483061 GSS 05-OCT-2000 GSSS.
NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was FCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-72871, and 72906-731399, Subtraction by Bento Soares and M. Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butleriae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)
10 (bases 1 to 19)
11 (bases 1 to 19)
12 (bases 1 to 19)
13 (bases 1 to 19)
14 (bases 1 to 19)
15 (bases 1 to 19)
16 (bases 1 to 19)
17 (bases 1 to 19)
18 (bases 1
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/lab_host="No. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57bi/60 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 6.9e+05;
0; Mismatches 1;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0119 row: I column: 23
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .19
/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xxef="taxon:10090"
/clone="UUGCIM0119123"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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AUTHORS
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LOCUS
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KEYWORDS
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/do type="mRNA"

/db Xref="type="mRNA"

/db Xref="type="mRNA"

/clone="IMAGE:2359240"

/clone lib="Suprass NFL T GBC S1"

/clone lib="Sorgan: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco R1; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gane Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
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19 bp mRNA linear EST 19-DEC-19
WF52e05.x1 Soares_NFL_T_GBC_S1 Homo saphens GDNA clone
IMAGB:2359240 3' similar to TR:Q39600 039600 EXTENSIN. ;contains
element MSR1 repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.

Trace considered overall poor quality
Insert Length: 724 Std Error: 0.00
Stg primer: -40UP from Gibco
High quality sequence stop: 1.

Location/Qualifiers
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Pred. No. 6.9e+05;
0; Mismatches 1;
      ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                    1. .16
/organism="Homo sapiens"
                                                             Trace considered overall poor qu
Insert Length: 353 Std Error:
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
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AI807936.1 GI:5394502
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91.7%;
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Homo sapiens
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Matches 11; Conserv
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AI807936/c
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil 4722114 | gb | AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ447936 1002 19 bp DNA linear GSS 04-OCT-2000 UM0245018F Mouse 1000 plasmid UUGCIM library Mus musculus genomic clone UUGCIM0245018 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/clone_lib="Mouse_lokb plasmid UGGCIM_library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (Malle) was obtained from the Jackson
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Pred. No. 6.9e+05;
0; Mismatches 1; Indels C
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: O column: 18
Seq primer: CGTTGTAAAACGACGCCAGT
class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/60"
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/clone="UUGC1M0245018"
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     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMn42 (g1|4732114|gb|ART129072.1), a -copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-comperent E. coli X110-Gold (Stratagene) cells and selected for ampicilin resistance."
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 19)
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1M0138G01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0138G01 R, genomic survey sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0138 row: G column: 01
Seq primer: CACACAGGAAACAGGTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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/strain="C57BL/6J"
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clone="UUGC1M0138G01"
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l Similarity 91.7%;
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance."
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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 19)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

L Ungublished

Contact: Robert B. Weiss

University of Urah Genome Center

University of Urah Genome Center

University of Urah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZMOO18BO9F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0018B09 F, genomic survey sequence.
AZ780591.1 GI:12912422
GSS.
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/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                           86.7%; Score 10.4; DB 28; Length 19; 91.7%; Pred. No. 6.9e+05;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 018 row: B column: 09
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0018B09"
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Location/Qualifiers
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Best Local Similarity
Matches 11; Conserv
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COMMENT
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AZ780591
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polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high morlar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732144 gb) hR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 bp DNA linear GSS 16-FEB-2001
2M0031B17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0031B17 R, genomic survey sequence.
A2786308.1 GI:12923936
GSS.
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Mus musculus
Mus musculus
Mus repeased Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
Mouse whole genome scaffolding with paired end reads from 10kb
Dlasmid inserts
Unpublished
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculs C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Pred. No. 6.9e+05;
0; Mismatches 1; Indels (
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C578L/60"
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/clone="UUGC2M0031B17"
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Fax: 801 585 7177
Email: ddunn@genet
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Best Local Similarity
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84112, US
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AZ786308
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us-09-331-204a-13.sz1m22.rst

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/lab host="B. Coli strain XLIO-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
musculus C57BL/G (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000 linear GSS 04-OCT-2000 LM0276J16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0276J16 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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  polymerase and T4
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Pred. No. 6.9e+05;
0; Mismatches 1; Indels (
was blunt end-repaired with T4 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: J column: 16
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Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/69"
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/clone="UUGC1M0276J16"
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                                   91.7%;
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Best Local Similarity 91.7
Matches 11, Conservative
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Fax: 801 585 7177
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COMMENT
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AZ466238
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was blunt end-repaired with T4 DNA polymerase and T4 and T6 polymerase and T6 polymerase to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored to remically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Muscaryotas, Metazoa, Chordata, Craniata, Vertebrata, Eutheleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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University of Utah Genome Center
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S.
84112, USA
Tel: 801 S85 5606
Fax: 801 S85 5707
Email: ddunn@genetics.utah.edu
Insert Lenghr: 1000 Std Error: 0.00
Plate: 0331 row: H column: 02
Seq primer: CACACAGGAAACAGCTATGACC
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Pred. No. 6.9e+05;
0; Mismatches 1;
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/mol_type="genomic DNA"
/strain="C57BL/63"
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/clone="UUGC1M0331H02"
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Location/Qualifiers
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Homo sapiens
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-complement.
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Unpublished
Contact: Robert B. Weiss
University of Utah
University of Utah
Pm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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2M0004G14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Mus musculus
Mus musculus
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert_Length: 10000 Std Exror: 0.00
Plate: 0004 row: G column: 14
Seg primer: CGTTGTAAAACGACGGCCAGT
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AZ774703.1 GI:12900261
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ONE WAY MATCH | Wow, Interpolymanically sheared by repeated passage through a not belong the property sheared by repeated passage through a not binner end-repaired with 14 DAA polymerase and 74 polymatestic defautases, adapter oligonatic colors and 74 polymatestic defautases and 74 polymatestic defautases, adapter oligonatic colors and 74 polymatestic defautases, an
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us-09-331-204a-13.szlm22.rst

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/clone="UdocIMUD84AD3"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/note="Wedcor: PWA2TW, Purified genomic DNA from M.
/note="Wedcor: PWA2TW, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMA2 (dil 47921H [dp] APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases 1 to 2.)

Dunn, D., Aoyad, A.)

Eslam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
1MO564A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
2clone UUGC1M0564A03 R, genomic survey sequence.
AZ766712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Insert Length: 1000 Std Error: 0.00
Plate: 0564 row: A column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol type="genomic DNA"
/strain="c57BL/60"
/db xref="taxon:10090"
/clone="UUGCINO564A03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                 Mus musculus (house mouse)
                                                                        AZ766712.1 GI:12884063
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AZ769521/c
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                                                                                                                                                                                                                                                                                                                                                                            22 bp mRNA linear EST 09-MAR-1999 ti5402.x1 NCI CGAP LYM12 Homo sapiens cDNA clone IMAGE:2134250 3/ similar to TR:\(\overline{Q}\)17089 COLLAGEN ;contains element MER22 A1439277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Enail: egapbs.r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAPP clone distribution information can be
found through the I.M.A.G.E. Consortim/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sal1; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dr. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
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/mol_type="mkype"
/mol_type="lymype"
/db xref="taxon:9606"
/clone="IMAGE:2134250"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHijay." 0 g 2 t
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Pred. No. 7e+05;
0; Mismatches 1;
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A4928040 119 bp mRNA linear EST 22-APR-1998 cols6969.3 NCI CGAP HN4 Homo sapiens cDNA clone IMAGE:1486912 3' similar to TR:004216 EXTENSIN; contains element MSR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contract: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Thissue Procurement: John Ensley, M.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 19)

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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/clone="IMAGE:1486912"
                                                                                                                                           AA928040
AA928040.1 GI:3077196
                                                                                                                                                                                                                      Homo sapiens (human)
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        GSS 16-FEB-2001
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 22)

Dunn, D., Adoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
AZ769521
1M0570018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10.4; DB 28; Length 22;
Pred. No. 7e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Exror: 0.00
Plate: 0570 row: 0 column: 18
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0570018"
                                                                                                              AZ769521.1 GI:12889741
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91.78;
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Fax: 801 585 7177
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ORIGIN
                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                            DEFINITION
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AUTHORS
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COMMENT
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/tissue_type="squamous cell carcinoma"
/lab host="SOLR (kanamycin resistant)"
/lab host="SOLR (kanamycin resistant)"
/clone="Organ: plarynx, Vector: Bluescript SK-; Site_1:
Foor: Site_2: Xhoi; Cloned unidirectionally. Primer:
Digo dr. Average insert size 1:5 kb. 5' adaptor sequence:
GAATTCGGCAGGA3 3' adaptor sequence: 5' GAATTCGGAGGTTTTTTTTTTTTTTTTT 3'"
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                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1e+06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           completed: October 27, 2003, 13:59:29
ne : 1055.51 secs
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100.0%; Pre
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Gaps

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11; Conservative

Matches

Similarity

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2, Appli
13, Appli
31, Appl
174, Appl
20, Appl
22, Appl
22, Appl
174, App
10, Appl
10, Appl
10, Appl
10, Appl
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                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08529878B

Patent No. 593256

GENERAL INFORMATION:
APPLICANT: Tam, FODER C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-5EP-1995
CLASSIFICATION: A 24
ATTORNEY/AGENT INFORMATION:
NAME: Fish, ROBERT D.
REGISTRATION NUMBER: 33,880
RESERRENCE/DOCKET UNIMBER: 213/003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 12; DB 2; L
larity 100.0%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 0;
US-09-429-130-11
PCT-US96-11786-11
PCT-US94-06431A-22
US-08-469-802B-13
US-08-469-802B-13
US-09-487-368A-174
US-09-62-249A-22
US-09-62-249A-22
US-09-62-249A-21
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US-09-62-644A-174
US-09-62-644A-174
US-09-198-452A-190
US-08-198-452A-100
US-08-198-168-100
US-08-535-168-100
US-08-535-100
US-09-01-974-100
US-08-535-100
US-08-535-100
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
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     GGGGTGGTGGGG
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Best Local Similarity
Matches 12; Conserv
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US-08-529-878B-3
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                                                                                  October 27, 2003, 10:32:34; Search time 27.5429 Seconds (without alignments) 192.304 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10,
Sequence 44,
Sequence 48,
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1: /cgn2 6/ptodate1/lina/5A_COMB.seq:*
    /cgn2 6/ptodate1/lina/5B_COMB.seq:*
3: /cgn2 6/ptodate1/lina/6A_COMB.seq:*
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5: /cgn2 6/ptodate1/lina/PCTUS_COMB.seq:*
6: /cgn2 6/ptodate1/lina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-529-878B-14
US-08-529-878B-44
US-08-529-878B-45
US-08-529-878B-45
US-09-017-974-65
US-09-017-974-65
US-09-017-974-65
US-08-682-255A-64
US-08-682-255A-64
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US-08-682-255A-65
US-08-802-255A-65
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US-09-429-130-65
US-09-429-130-65
US-09-031-65
US-08-890-979-56
US-08-890-979-56
US-08-890-979-56
US-09-031-626-56
US-08-145-704-11
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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12
1 9999t99t9999 12
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Match Length DB
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Maximum DB seq length: 22
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Perfect score:
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                                                                                                                                                                   Sequence:
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WESULY 4

WESULY 4

WESULY 4

Sequence 48, Application US/08529878B

FACTOR NO. 829256.

FACTOR S032586.

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
ADDRESSE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
ZIP: 90618.

COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC Compatible
COMPUTER: IBM PC COMPATA:

APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION NUMBER: 33,880

REGISTRATION NUMBER: 33,880

REFERENCE/DOCKET NUMBER: 213/003
TELEBROME: 714-525-3303
TELEBRAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 12; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRONE: 714-525-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-44
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
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TOPOLOGY: ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-529-878B-48
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                                                                                                                              GENERAL INFORMATION:

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
ITILE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
ADDRESSES: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra.
STREET: 3000 S. Augusta Court
CITY: La Habra.
STATE: California
STATE: California
COUNTRY: United States of America
ZIP: 90631
COMPUTER: United States of America
STATE: MEDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
TELECOMMUNICATION NUMBER: 213/003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/08529878B
Patent No. 5932556
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCES: 48
CORRESPONDENCE ADDRESS: Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
STATE: Godding States
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: TIMP PC compatible
COMPUTER: PINR PC compatible
                                                            US-08-529-878B-10/c; Sequence 10, Application US/08529878B; Patent No. 5932556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gegereereege 12
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TELEX:
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Patent No. 6288042

GENERAL INFORMATION:
PAPPLICANT: Rando, Robert F.
APPLICANT: Hogan, Michael E.
APPLICANT: Wallace, Thomas L.
APPLICANT: Wallace, Thomas L.
APPLICANT: Wallace, Thomas L.
APPLICANT: Wallace, Thomas L.
APPLICANT: TILE OF INVENTION: Anti-viral Guanosine-Rich
ITILE OF INVENTION: Terrad Forming Oligonuclectides
NUMBER OF SEQUENCES AB
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 12; DB 2; 100.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: 1.8.A.

ZIP: 77002-2912

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                         COMPUTER: REALPE FORDY disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANGE: 714-525-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Conley, Rose & Tayon, P.C. 600 Travis, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICALL.
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,374
FILING DATE: 04-FBB-97
APPLICATION NUMBER:
FILING DATE: 09-DEC-97
ATTORNEY/AGENT INFORMATION:
WAME: McDaniel, C. Steven
                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
US-08-529-878B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 21 base pairs
TYPE: nucleic acid
            COUNTRY: United Stat
ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 600 Tre
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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0
                                                                                                                     Length 21;
                Pred. No. 1.1e+03;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/08529878B
Patent No. 5932556
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 12; DB 2; Best Local Similarity 100.0%; Pred. No. 1.1e+03 Matches 12; Conservative 0; Mismatches (
100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY unknown ; MOLECULE TYPE: DNA (genomic) US-08-529-878B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4 SEQUENCE FERRACTERSITICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
            Best Local Similarity 100.
Matches 12; Conservative
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                                                                1 GGGGTGGTGGGG 12
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                                                                                               18 GGGGTGGTGGGG 7
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Gaps
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                Length 17;
                                                                                                                                                                                                                                                                              RESULT 9

US.09-017-974-65

i Sequence 65, Application US/09017974

j Sequence 65, Application US/09017974

j Sequence 65, Application US/09017974

j Settle No. 6288042

general information Robert F.

APPLICANT Rando, Robert F.

APPLICANT Hogan, Michael E.

APPLICANT Hogan, Michael E.

APPLICANT HOSSUM, Mallac, Paul A.

TITLE OF INVENTION: Anti-Viral Guancsine-Rich

TITLE OF INVENTION: Anti-Viral Guancsine-Rich

TITLE OF INVENTION: Anti-Viral Guancsine-Rich

TITLE OF INVENTION: Actival Forming Oligonucleotides

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STATE: Texas

COUNTRY: US.A.

ZIP: 7002-2912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%; Score 11; DB 3; Lv
100.0%; Pred. No. 3.3e+03;
tive 0; Mismatches 0;
                Score 11; DB 3; L
; Pred. No. 3.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: MS word 97 (saved as .txt file)
SOFTWARE: MS word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,974
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,374
FILING DATE: 04-FEB-97
APPLICATION NUMBER: 60/037,374
FILING DATE: 09-DEC-97
ATTORNEY/AGENT INPORMATION:
NAME: MCDAINEI, C. STEEVEN
REGERENCE/DOCKET NUMBER: 1472-06223
REFERENCE/DOCKET NUMBER: 1472-06223
TELEPHONE: 713/239-8010
TELEPHONE: 713/239-8010
TELEPHONE: 713/239-8010
TELEPHONE: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 5
OTHER INFORMATION: /note= "C-5 propynl dU"
91.7%; Sco...
100.0%; Pred. No. s...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear (OLECULE TYPE: DNA (genomic)
                Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11, Conservative
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Matches 11; Conserv
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| Sequence 64, Application US/09017974 |
| GENERAL INFORMATION: And Obsert F. APPLICANT: Rando, Robert F. APPLICANT: Hogan, Michael B. APPLICANT: Mallace, Thomas L. APPLICANT: Mallace, Thomas L. APPLICANT: Gosum, Michael B. APPLICANT: Cosum, Mallace, Terad Forming Oligonuclectides CORRESPONDENCE ADDRESS: 86 |
| CORPUTER: TEAMS COMPATION: Suite 1800 |
| CITY: Houston Compatible Compatible CORPUTER: IBM PC Compatible COMPUTER: IBM PC COMPATION: SUITE TOPPY disk COMPUTER: IBM PC COMPATION: SOURTWARE IS TOPPY disk COMPUTER: IBM PC COMPATION: APPLICATION NUMBER: 05/09/017,974 |
| FILING DATE: 04-FEB-97 |
| REGISTRANDION NUMBER: 133-962 |
| REDECOMMUNICATION INFORMATION: TELEPHONE: 731-38-8001 |
| TELEFRAX: 713-738-8001 |
| TELEFRAX: 713-728-8001 |
| TELEFRAX: 713-738-801 |
| TELEFRAX: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
91.7%; Score 11; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels
            REGISTRATION NUMBER: 33,962
REFERENCE POCKET NUMBER: 1472-06223
TELECOMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEPHONE: 713/238-8010
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-09-017-974-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 dederrecraed 16
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RESULT 10

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                              APPLICANT: Zendegui, Joseph G. APPLICANT: Ojwang, Joshua O. APPLICANT: Ojwang, Joshua O. APPLICANT: Hogan, Michael E. APPLICANT: Pogmiler, Eyves APPLICANT: Pogmiler, Eyves APPLICANT: Pogmiler, Eyves APPLICANT: Maxumder, Abhijit TITLE OF INVENITON: Oligonucleotides G. APPLICANT: Wather Application and Congress of Correspondences: 87 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESSE: Conley, Suite 1850 CITY: Houston CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.3e+03;
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Pred. No. 3.3e+0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65, Application US/08682255A
Patent No. 6323185
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Rendewald, Susan
APPLICANT: Cendequi, Joseph G.
APPLICANT: Ojwang, Joshua O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%; SCCI
100.0%; Pre
0;
                        Fennewald, Susan
Zendegui, Joseph G.
Ojwang, Joshua O.
Hogan, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-682-255A-65
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            GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Rennewald, Susan
APPLICANT: Zendeguli, Joseph G.
APPLICANT: Pennewald, Susan
APPLICANT: Pomnier, Byese
APPLICANT: Pogan, Michael E.
APPLICANT: Pogan, Michael E.
APPLICANT: Pogan, Michael E.
APPLICANT: Pogan, Michael E.
APPLICANT: Pomnier, Eyves
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSES: Conley, Rose & TITLE
STREET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Houston
STATE: Texas
COUNTY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MADIUM TYPE: Eloppy disk
COMPUTER: IBM PC COMPACIALE
CONFUTER: IBM PC COMPACIALE
CONFUTER: IBM Nord 97 (acved as .tx file)
SOFWATING SYSTEM: MS WAID 97 (acved as .tx file)
SOFWATE: MS WORD 97 (acved as .tx file)
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,255A
FILING DATE: 17-UULY-1996
CLASSIFICATION NUMBER: US/08/535,168
FILING DATE: 19-UULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 19-UULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 19-UARCH-96
APPLICATION NUMBER: 60/015,714
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,714
FILING DATE: 23-MARCH-96
APPLICATION NUMBER: 60/016,714
FILING DATE: 23-MARCH-96
APPLICATION NUMBER: 60/016,714
FILING DATE: 23-APRLL-96
APPLICATION NUMBER: 60/016,714
FILING DATE: 33-APRLL-96
APPLICATION NUMBER: 60/016,714
FILING DATE: 33-APRLL-96
APPLICATION NUMBER: 33-962
REFERENCE/DOCKET NUMBER: 31,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELEPHONE: 713/238-8010
                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Conley, Rose & Tayon, P.C. 600 Travis, Suite 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 64, Application US/08682255A Patent No. 6323185
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INPORMATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS: LENGHT: 17 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGGTGGTGGG 11
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US-08-682-255A-64
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US-08-682-255A-62
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Length 17;
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COUNTRY: U.S.A.

ZUN: 77002-2912

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130

FILING DATE: 28-OCt-1999

CLASSIFICATION: CURRINGMD.
Hogan, Michael E.
Pommier, Eyves
Mazunder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/682,255
FILING DATE: CUNKNOWN PAPPLICATION NUMBER: 60/001,505
FILING DATE: 19-UULY-95
APPLICATION NUMBER: 60/013,686
FILING DATE: 25-WARCH-96
APPLICATION NUMBER: 60/013,686
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/013,686
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%; Score 11; DB 4;
100.0%; Pred. No. 3.3e+0
tive 0; Mismatches
                                                                                                                            NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSES: Conley, Rose & Tayon,
STREET: 600 Travis, Suite 1850
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ 1D NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APRIL-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application US/09429130
Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan
Zendegui, Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           near
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Best Local Similarity 100.
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US-09-429-130-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%; Score 11; DB 4; Le
100.0%; Pred. No. 3.3e+03;
tive 0; Mismatches 0;
                                                                                                                                                                       STREET: GOO Travis, Suite 1850
CITY: Houston
STATE: Texas.
COMPUTEY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS WINDOWS 95
SOFTWARE: MS WORD 97 (saved as .txt file)
COMPUTER: IDM PC compatible
OPERATING SYSTEM: MS WINDOWS 95
SOFTWARE: MS WORD 97 (saved as .txt file)
CURRENT APPLICATION DATA: MS WINDOWS 95
SOFTWARE: MS WORD 97 (saved as .txt file)
APPLICATION NUMBER: US 08/535,168
FILING DATE: 13-ULY-95
APPLICATION NUMBER: GO/01,505
FILING DATE: 19-WARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/015,714
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 33-962
REGISTRATION NUMBER: 33,962
REGISTRATION NUMBER: 1472-06214
TELEPHONE: 713/298-8010
APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Eyves
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-viral Guanosine-Rich
TITLE OF INVENTION: Oligonuclectides
NUMBER OF SEQUENCES: 87
ADDRESSEE: Conley, Rose & Tayon, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5
CTHER INFORMATION: /note= "C-5 propynl dU"
US-08-682-255A-65
                                                                                                                                                        3: Conley, Rose & Tayon, P.C. 600 Travis, Suite 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-09-429-130-62
; Sequence 62, Application US/09429130
; Patent No. 6355785
; GENERAL INFORMATION:
. APPLICANT: Rando, Robert F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fennewald, Susan
Zendegui, Joseph G.
Ojwang, Joshua O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 713/228-8008
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGTGGTGGG 16
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Best Local Similarity
Matches 11; Conserva
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER_INFORMATION: /note= "C-5 propynl dU" sequence Description: seq ID NO: 65: US-09-429-130-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible.
COMPUTER: IBM PC compatible.
COMPATION SYSTEM: MS Windows 95
CURRENT APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 28-Oct.-1999
CLASSIFICATION: <a href="https://doi.org/10.00/10.00/">CURRENT APPLICATION NUMBER: US/09/429,130</a>
CLASSIFICATION: <a href="https://doi.org/">CURRENT APPLICATION: <a href="https://doi.org/">CURRENT APPLIC
                                                                Hogan, hadden, Byves
Pommier, Eyves
Mazumder, Abhijit
62(015,714
TITLE OF INVENTION: Anti-Viral Guancsine-Rich
Oligonucleotides
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
CONNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: «UNKNOWN»

APPLICATION NUMBER: 60/001,505

FILING DATE: 19-JULY-95

APPLICATION NUMBER: 60/014,007

FILING DATE: 25-WARCH-96

APPLICATION NUMBER: 60/013,688

FILING DATE: 19-WARCH-96

APPLICATION NUMBER: 60/016,271

FILING DATE: 17-APPLL-96

ATTORNEY/AGENT INFORMATION:

NAME: McDatalon NUMBER: 33,962

REFERENCE/DOCKET NUMBER: 1472-06214

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: October 27, 2003, 14:03:36 Job time : 28.5429 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/682,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APRIL-96
        Zendegui, Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                            Ojwang, Joshua O.
Hogan, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGGTGGG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: 14.8.A.

ZIP: 71002-2912

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS WORD 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <underween
Ojwang, Joshua O.
Hogan, Michael B.
Pommier, Eyves
Mazumder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/682,255
FILING DATE: cUnknown
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-UUJY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRL-96
APPLICATION NUMBER: 33,962
REGISTATION NUMBER: 31,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSES: Conley, Rose & Tayon,
STREET: 600 Travis, Suite 1850
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLGGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-APRIL-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 55, Application US/09429130
Patent No. 635785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Texas
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US-09-429-130-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-429-130-64
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-09-740-332-2132/c
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

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5: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1792395 segs, 1340900451 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                         US-09-331-204A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 22
                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                              OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Core Match Length DB ID Description

No. Score Match Length DB ID Description

C 1 12 100.0 17 11 US-09-740-332-2132 Sequence 2132, Ap 2 12 100.0 17 11 US-09-740-332-2133 Sequence 2133, Ap 2 12 100.0 17 11 US-09-740-332-2423 Sequence 2422, Ap 2 12 100.0 17 12 US-09-917-879-2132 Sequence 2422, Ap 2 12 100.0 17 12 US-09-917-879-2132 Sequence 2422, Ap 2 12 100.0 17 12 US-09-817-879-2132 Sequence 2422, Ap 2 12 100.0 17 12 US-09-817-879-2132 Sequence 2422, Ap 2 11 10.0 17 12 US-09-817-879-2132 Sequence 2422, Ap 2 11 10.1 10.1 12 US-09-817-879-2133 Sequence 2422, Ap 2 11 10.1 10.1 12 US-09-179-152-56 Sequence 39, App1 C 11 11 91.7 20 11 US-09-779-152-56 Sequence 56, App1 C 12 US-10-184-085A-365 Sequence 366, App C 13 11 91.7 21 US-10-184-085A-366 Sequence 366, App C 15 11 91.7 21 US-10-184-085A-368 Sequence 367, App C 15 11 91.7 21 US-10-184-085A-368 Sequence 370, App C 16 11 91.7 21 US-10-184-085A-368 Sequence 370, App

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APPLICANT: Nibozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001.03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 2132
LENGTH: 17
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US-09-740-312-2133/c
US-09-740-312-2133/c
; Publication No. US2003012527081
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION:
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llarity 100.0%; Pred. No. 9e+03;
Conservative 0; Mismatches 0;
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US-09-740-332-2132
Sequence 2132, Application US/09740332 Publication No. US20030125270A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: artificial sequence
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Best Local Similarity
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Sequence 2133, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Bnzymatic Nucleic Acid Treatment of Diseases or Conditions Rela:
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION WUMBER: US/09/817,879
CURRENT PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 2133
LENGTH: 17
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US-09-817-879-2132/c

US-09-817-879-2132/c

Sequence 2132, Application US/09817879

Publication No. US20030171311A1

GENERAL INFORMATION:

APPLICANT: Ribozyme bharmaceuticals Inc.

TITLE OF INVENTION: Hepatitis C Virus Infection

CURRENT PELLICATION NUMBER: US/09/817,879

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9703

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2132
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100.0%; Score 12; DB 11;
Best Local Similarity 83.3%; Fred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0;
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100.0%; Pred. No. 9e+03;
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Pred. No. 9e+03;
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; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133
                                                                           LOCATION:
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate US-09-740-332-2423
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       ORGANISM: artificial sequence
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Best Local Similarity
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US-09-817-879-2133/c
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Publication No. US20030125270A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C virus Infection
TITLE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 2423
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Publication No. US20030125270A1
Publication No. US20030125270A1
Publication No. US20030125270A1
Publication No. US20030125270A1
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Broymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: RPI 400/03
CURRENT APPLICATION WUMBER: US/09/740,332
CURRENT TILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin Version 3.0
LENGTH: 17
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83.3%; Pred. No. 9e+03;
cive 2; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 12; Conservative 0; Mismatches 0;
TITLE OF INVENTION: Hepatitis C Virus Infection FILE REFERENCE: RPI 400/003 CURRENT APPLICATION NUMBER: US/09/740,332 CURRENT FILING DATE: 2001-03-26 NUMBER OF SEQ ID NOS: 9704 SOFTWARE: Patentin version 3.0 LENGHH: 17
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                                                                                                                                                                                                            TYPE: RNA
ORGANISM: artificial seguence
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ORGANISM: artificial sequence
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Matches 10; Conservative
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US-09-740-332-2422
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| Publication No. US20030044782A1
| GENERAL INFORMATION:
| APPLICANT: Acton, Susan L.
| TITLE OF INVENTION: DIANOCSTIC ASSAYS AND KITS FOR BODY MASS AND ITLE OF INVENTION: CARDIOVASCULAR DISORDERS
| TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
| TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
| TILLE REFERENCE: MNI-172CP2
| CURRENT APPLICATION NUMBER: US/09/779,152
| CURRENT FILING DATE: 1997-07-10
| NUMBER OF SEQ ID NOS: 121
| SOFTWARE: PatentIn Ver. 2.0
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Sequence 39, Application US/10148687
Publication No US20030185836A1
GENERAL INPORMATION.
APPLICANT: WINDER, Gerhard
APPLICANT: WILLIAMS, Keith Leslie
APPLICANT: WILLIAMS, Keith Leslie
APPLICANT: WILLIAMS, Keith Leslie
APPLICANT: Wadrew Arthur
APPLICANT: Cryptosporidium sporozoite antigens
FILE REPRENCE: 047763-5019-US
CURRENT FILING DATE: 2000-12-01
FRIOR APPLICATION NUMBER: PCT/AU00/01492
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 1099-12-01
PRIOR FILING DATE: 1999-12-01
SEQ ID NO 39
LENGTH: 19
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100.0%; Pred. No. 2.5e+04;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial COTHER INFORMATION: Oligonucleotide primers US-10-148-687-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 56, Application US/10023610; Publication No. US20030023059A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11, Conservative
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CRGANISM: Human
US-09-779-152-56
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US-09-779-152-56/c
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US-10-023-610-56/c
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                                                                                                                                                                                                   Sequence 2422, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Bazymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: US/09/817,879
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2422
ILENGTH: 17
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Sequence 2423, Application US/09817879
Sequence 2423, Application US/09817879
Sequence 2423, Application US/09817879
Sequence 2423, Application US/09171311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING BATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
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               Indels
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            Mismatches
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ORGANISM: artificial sequence
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Best Local Similarity 83.3
Matches 10; Conservative
          12; Conservative
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                                                         1 GGGGTGGTGGGG 12
                                                                                                    13 GGGGTGGTGGGG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-817-879-2422
                                                                                                                                                                                                 US-09-817-879-2422
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US-10-148-687-39/C
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LENGTH: 17
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          Matches
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LENGTH:

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Publication No. US20030152950A1
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Lalog, Robert P.
TITLE OF INVENTION Identification of Chemically Modified Polymers
TITLE OF INVENTION NUMBER: US/10/184,085A
CURRENT FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 1291
SEQ ID NO 367
LENGTH: 21
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-184-085A-368/c

| US-10-184-085A-368/c
| Sequence 368, Application US/10184085A
| Publication No. US20030152950A1
| GENERAL INFORMATION:
| APPLICANT: Garner, Harold R.
| APPLICANT: Garner, Harold R.
| APPLICANT: Balog, Kevin, J.
| APPLICANT: Balog, Robert P.
| APPLICANT: 119929-1035
| CURRENT APPLICATION NUMBER: US/10/184,085A
| CURRENT APPLICATION NUMBER: US 60/301,370
| PRIOR FILING DATE: 2001-06-27
| NUMBER OF SEQ ID NOS: 1291
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 2.5e+04;
cive .0; Mismatches 0;
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       PRIOR APPLICATION NUMBER: US 60/301,370
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 1291
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 366
LENGTH: 21
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-184-085A-366
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) ORGANISM: Homo sapiens
US-10-184-085A-367
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Matches 11, Conserv
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US-10-184-085A-367/c
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APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Buebke, Kevin, J.
APPLICANT: Balogy Robert P.
TITLE OF INVENTION: Identification of Chemically Modified Polymers
FILE REFERENCE: 119929-1035
CURRENT APPLICATION NUMBER: US/10/184,085A
CURRENT APPLICATION NUMBER: US 60/301,370
PRIOR PPLING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 1291
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
CREATH: 21
TYPE: DNA
TYPE: DNA
CREATH: 21
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Publication No. US20030152950A1
GENERAL INFORMATION.
APPLICANT: Garner, Harold R.
APPLICANT: Minna, John D.
APPLICANT: Luebke, Kevin, J.
APPLICANT: Balog, Robert P.
TITLE OF INVENTION: Identification of Chemically Modified Polymers
FILE REPERENCE: 119929-1035
CURRENT APPLICANTON VURBER: US/10/184,085A
CURRENT FILING DATE: 2002-10-01
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APPLICANT: Acton, Susan L.

TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
FILE REFERENCE: MIA-005.03
CURRENT APPLICATION NUMBER: US/10/023,610
CURRENT FILING DATE: 2001-12-17
EAALIER APPLICATION NUMBER: 09/686,106
EAALIER APPLICATION NUMBER: 09/032,894
EAALIER FILING DATE: 1996-02-27
EAALIER FILING DATE: 1996-02-27
EAALIER FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PALENTIN Ver. 2.0
SOFTWARE: PALENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11; DB 14; Length 20;
Pred. No. 2.5e+04;
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100.08;
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-184-085A-366/c
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US-10-184-085A-365/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-10-023-610-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-184-085A-365
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: October 27, 2003, 19:00:53 Job time : 258.629 secs

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/ptodata/1 /ptodata/1 /ptodata/1 ptodata/: ptodata/:

ptodata/ otodata/

otodata, todata/ ptodata, codata, COMB. seq: *

/pna/US6018 pna/US6017

> odata/ codata/ todata/

/pna/US6012 /pna/US6013 pna/US6015 pna/US6016

> codata/ codata/ ptodata/ codata/

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ptodata/

COMB.seq:*

pna/US6020 pna/US6021

codata/

todata/

COMB. seg: COMB. seq:*

/pna/US6023A_C/pna/US6023B_C/pna/US6024_CC

pna/US6025

todata/

otodata/

Run on:

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, Search time 1570.86 Seconds (without alignments) 253.343 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*

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4: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

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7: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

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15: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

16: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

16: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

16: /cgn2_6/ptodata/1/pna/USOB_COMB.seq:*

17: /cgn2_6/ptodata/1/pna/USOBA_COMB.seq:*

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19: /cgn2_6/ptodata/1/pna/USOBA_COMB.seq:*

10: /cgn2_6/ptodat
GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                October 27, 2003, 10:32:35 ;
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 22
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Description		Sequence 13, Appl	Sequence 49, Appl	Sequence 49, Appl
ΔI	12 19 US-09-331-204-3	US-09-331-204A-13	PCT-US01-21306-49	PCT-US01-21306-49
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% Query Match Length DB ID	12	12	15	15
% Query Match	100.0	100.0	100.0	100.0
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Result No.	1	2	m	4,

SUMMARIES

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100.0%; Score 12; DB 1; Length 15; 100.0%; Pred. No. 8.7e+04;
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100.0%; Pred. No. 8.7e+04;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bentivegna, Steven C
APPLICANT: Bentivegna, Steven C
APPLICANT: Bentivegna, Steven C
APPLICANT: Bleglecki, Karyn M.
APPLICANT: Kazemi, Ameni
APPLICANT: Kazemi, Ameni
APPLICANT: Kazemi, Ameni
APPLICANT: Koshy, Beena
ITLE OF INVENTION: Haplotypes of the ETFB Gene
ITLE REFERENCE: MWH-0902PCT ETFB
CURRENT APPLICATION NUMBER: 60/215,984 FILMS PATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/215,984 PRIOR PLING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 49
LENGTH: 15
       Mismatches
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PCT-0501-21306-49
PCT-0501-21306-49
Requence 49, Application PC/TUS0121306
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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       12; Conservative
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CRGANISM: Homo sapiens
PCT-US01-21306-49
       Matches
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   Sequence 2132, Ap Sequence 2423, Ap Sequence 10, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 24, Appli Sequence 21313, A Sequence 22, Appli Sequence 64, Appli Sequence 64, Appli Sequence 62, Appli Sequence 62, Appli Sequence 62, Appli Sequence 64, Appli Sequence 62, Appli Sequence 64, Appli Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09331204
GENERAL INFORMATION:
APPLICANT: Tam, Robert
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-RICH OLICO APPAMERS AND METHODS OF MODULATING AN TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: An oligomer
OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
OTHER INFORMATION: acid. This term includes oligomers consisting of
CTHER INFORMATION: acid. This term includes oligomers consisting of
US-09-331-204-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 19; Length 12;
Pred. No. 8.7e+04;
100.0%;
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Best Local Similarity
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APPLICANT: Genaissance Pharmaceuticals, Inc.

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APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relativities of INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION WUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
LENGTH: 17
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TITLE OF INVENTION: Brzymatic Nucleic Acid Treatment of Diseases or Conditions Relativities OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION UNMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 422
LENGTH: 17
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Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0;
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Best Local Similarity 83.3%; Pred. No. 8.7e+04;
Matches 10; Conservative 2; Mismatches 0;
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Best Local Similarity 83.3%; Pred. No. 8.7e+04;
Matches 10; Conservative 2; Mismatches 0;
                                   ; FEATURE:

NAME/KEY: misc_feature

; LOCATION:

; OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-2133
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; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2422
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, OTHER INFORMATION: oligonucleotide substrate US-09-740-332-2423
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ORGANISM: artificial sequence
               ORGANISM: artificial sequence
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NAME/KEY: misc_feature
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US-09-7-40-332-2132/C
US-09-7-40-332-2132/C
Sequence 2132, Application US/09740332
GENERAL INFORMATION:
FARE APPLICAMY: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT APPLICATION NUMBER: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: ParentIn version 3.0
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GENERAL INFORMATION:
APPLICAMY: Rabozyme Pharmaceuticals Inc.
APPLICAMY: Rabozyme Pharmaceuticals Inc.
APPLICAMY: Rabozyme Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Braymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C virus Infection
CURRENT APPLICATION WINDER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: ParentIn version 3.0
SEQ ID NO 2133
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APPLICANT: Bentivegna, Steven C
APPLICANT: Bieglecki, karyn M.
APPLICANT: Kazemi, Amir
APPLICANT: Kazemi, Amir
APPLICANT: Koshy, Beena
TITLE OF INVENTION: Haplocypes of the ETFB Gene
FILE REFERENCE: WHH-0902PCF ETFB
CURRENT APPLICATION NUMBER: PCT/US01/21306
CURRENT FILING DATE: 2001-07-06
PRIOR PPLING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 141
SOFTWARE: Patentin Ver. 2.1
SSOFTWARE: Patentin Ver. 2.1
LENGTH: 15
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Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 12; DB 2; I
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0;
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ORGANISM: artificial sequence
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; ORGANISM: Homo sapiens
PCT-US01-21306-49
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US-09-740-332-2133/c
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RESULT 12
US-09-1423
US-09-17-17
US-09-17-17
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozymaceuticals Inc.
TITLE OF INVENTION: Braymatic Nucleic Acid Treatment of Diseases or Conditions Rela:
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBH800-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
UNDERROY APPLICATION NUMBER: US/09/817,879
UNDERROY SEQ ID NOS: 9703
SEQ ID NO 2423
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TITLE OF INVENTION:
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83.3%; Pred. No. 8.7e+04;
iive 2; Mismatches 0;
TITLE OF INVENTION: Hepatitis C Virus Infection FILE REFERRICE: MBHB00-801-F CURRENT APPLICATION NUMBER: US/09/817,879 CURRENT FILING DATE: 2001-03-26 NUMBER OF SEQ ID NOS: 9703 SOFTWARE: Patentin version 3.0 SEQ ID NO 2422 LENGTH: 17
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; LOCATION:
; OTHER INCEMATION: oligonucleotide substrate
US-09-817-879-2422
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ORGANISM: artificial sequence
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Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-10-303-778-13820
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LOCATION:
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US-10-303-778-13820
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GENERAL INFORMATION:
TRIBOSYME PLARMACEULICALS AND TROUGHT STRONG SEQUENCE AND TROUGHT STRONG SEQUENCE AND TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
LENGTH: 17
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US-09-817-879-2133/c
US-09-817-879-2133/c
GENERAL INFORMATION:
FAPPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatities C Virus Infection
TITLE OF INVENTION: WHEBO. 801-F
TITLE REFERENCE: WHEBO. 801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
FEMALE OF SEQ ID NOS: 9703
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
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100.0%; Pred. No. 8.7e+04;
cive 0, Mismatches 0;
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; LOCATION:
; OTHER
US-09-817-879-2132
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|GGGUGGUGGGG 14
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Matches 12; Conserv
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                                COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: I'M PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,041A
FILING DATE: 12-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGNYI INFORMATION:
NAME: HAILUM, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 825.011
TELEPHONE 415-854-366
TELEPHONE: 415-854-366
TELEPHONE: 415-854-369
TELEPHONE: GHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNES: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 12;
100.0%; Pred. No. ative 0; Mismatch
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United States of America
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Best Local Similarity 100.
Matches 12, Conservative
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                                                                                                                                                                                                                                                                  Sequence 3, Application US/08387041A

GENERAL INFORMATION:
APPLICANT: Tam, Robert C
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
TITLE OF INVENTION: OF CD28 EXPRESSION
TITLE OF SEQUENCES:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUMTRY: United States of America
STRATE: New York
COUMTRY: United States of America
STRET: New York
COUMTRE: PEDDPY disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: PLODS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/387,041A
ATTORNEY/AGENT INFORMATION:
REFINENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
TELEPHONE: 415-884-3694
TELEPHONE: 415-884-3694
TELEPHONE: 415-884-3694
TELEPHONE: GALARACTERISTICS:
LENGTH 18 base pairs
TYPE: INICIPATION CARE
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Sequence 10, Application US/08387041A
GENERAL INFORMATION:
APPLICANT Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                 100.0%; Score 12; DB 50; Length 17; 100.0%; Pred. No. 8.7e+04; ive 0; Mismatches 0; Indels
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100.0%; Score 12;
Best Local Similarity 100.0%; Pred. No. 6
Matches 12; Conservative 0; Mismatche
            Query Match
Best Local Similarity 100.
Matches 12; Conservative
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Gaps

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Sequence 46976, A Sequence 4188, A Sequence 71313, A Sequence 71313, A Sequence 72837, A Sequence 42141, A Sequence 10573, A Sequence 55500, A Sequence 22, Appl Sequence 78687, A Sequence 7868
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Sequence 4726, Ap
Sequence 5015, Ap
Sequence 5016, Ap
Sequence 9770, Ap
Sequence 97857, A
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                                                                                                                                                                                                          October 27, 2003, 11:09:34 ; Search time 204.686 Seconds (without alignments) 97.777 Million cell updates/sec
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(cgn2_6/ptodata11/pna/USO6_NEW_COMB.seq:*

(cgn2_6/ptodata11/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata11/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata11/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata11/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata11/pna/USO0_NEW_COMB.seq:*

(cgn2_6/ptodata11/pna/USO0_NEW_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-669-841-5015

US-10-669-841-5015

US-10-669-841-5015

PCT-USO2-38216-9770

PCT-USO2-38216-7885

PCT-USO2-38216-7885

PCT-USO2-38216-7885

PCT-USO2-38216-7885

PCT-USO2-38216-78876

PCT-USO2-38216-78876

PCT-USO2-38216-78876

PCT-USO2-38216-78761

PCT-USO2-38216-78761
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PCT-US02-38216-64022
US-09-978-333B-2
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 22
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
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333C-2	PCT-US02-38216-39252	PCT-US02-38216-63970	PCT-US02-38216-83087	PCT-US02-38216-34808	PCT-US02-38216-72787	PCT-US02-38216-84942	PCT-US02-38216-84968	PCT-US02-38216-9718	PCT-US02-38216-31332	PCT-US02-38216-51833	PCT-US02-38216-60635	PCT-US02-38216-61028	PCT-US02-38216-64024	PCT-US02-38216-72823	PCT-US02-38216-73073	PCT-US02-38216-75530	PCT-US02-38216-9811	PCT-US02-38216-26671
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91.7	91.7	91.7	91.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	9	86.7	86.7	86.7
11	11	11	11	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4
27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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Sequence 4122/C
Sequence 6122/C
Sequence 6122/
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APPLICANT: Rentach, Drager
APPLICANT: Rentach, Drager
APPLICANT: Rentach, Drager
APPLICANT: Rentach, Drager
APPLICANT: Elisabeth, Drager
APPLICANT: Elisabeth, Drager
TITLE OF INVENTION: OLIGONOCLECTION
TITLE OF INVENTION: OLIGONOCLECTION
TITLE OF INVENTION: VIROS REPLICATION
TITLE OF INVENTION: VIROS REPLICATION
TITLE OF INVENTION: VIROS REPLICATION
TITLE OF INVENTION: OLIGONOCLECTION
FRIEND APPLICATION NUMBER: US/002/09187
PRIOR PELING DATE: 2001-06-08
PRIOR PELING DATE: 2001-10-24
PRIOR PELING DATE: 2001-10-24
PRIOR PELING DATE: 2001-10-26
PRIOR PELING DATE: 2001-12-05
PRIOR PELING DATE: 2001-12-05
PRIOR PELING DATE: 2001-12-05
PRIOR PELING DATE: 2001-06-06
PRIOR PELING DATE: 2001-03-26
PRIOR PELING DATE: 2001-03-26
PRIOR PELING DATE: 2001-03-36
PRIOR PELING DATE: 2001-03-36
PRIOR PELING DATE: 2001-03-36
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-0
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2; Mismatches 0; Indels
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; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5016, Application US/10669841; GENERAL INFORMATION:
                                                                                                                                    , Sequence 5015, Application US/10669841
, GENERAL INFORMATION:
, APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sirna Therapeutics, Inc. APPLICANT: Lawrence, Blatt APPLICANT: Dennis, Macejak APPLICANT: James, McSwiggen APPLICANT: David, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                     Dennis, Macejak
James, McSwiggen
David, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                      Patrice, Lee
Kenneth, Draper
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                      Lawrence,
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Dennis, Macejak
APPLICANT: Patrice, Lee
APPLICANT: Marisey
APPLICANT: Wenneth, Drape:
APPLICANT: Marisey
APPLICANT: Wenneth, Drape:
APPLICANT: Marisey
APPLICANT: 
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                                                                                                                                 100.0%; Score 12; DB 6; Length 17; ilarity 100.0%; Pred. No. 1.4e+04; Conservative 0; Mismatches 0; Indels
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; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-4725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4726, Application US/10669841 GENERAL INFORMATION:
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ORGANISM: Artificial Seguence
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                               Best Local Similarity
Matches 12; Conserv
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US-10-669-841-4726/c
                                                                                                                                                    Query Match
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APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BENERAL SAND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 72857
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GENERAL INFORMATION:
APPLICAMY: ROSELTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENERAL AND USES THEREOF
TITLE OF INVENTION: GENERAL PROLICATION NUMBER: POT/USO2/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86641
SOFTWARE: PATENTIN VERSION 3.2
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GENERAL INFORMATION
APPLICANT: ROSetta Genomics LTD
TITLE OF INVENTION: GENERAL TICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENERAL AND USES THEREOF
TILE REPERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
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Gaps
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Indels
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Pred. No. 1.4e+04;
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Mismatches
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Best Local Similarity 100.
Matches 12, Conservative
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Best Local Similarity 100.
Matches 12; Conservative
12; Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-46976
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PCT-US02-38216-72857
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Matches
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   APPLICANT: Remeth, Drager
APPLICANT: Elisabeth, Roberts
APPLICANT: Elisabeth, Roberts
APPLICANT: OLIGONUCLECTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION: VIRUS REPLICATION
FILE PERERNCE: 400/042US (MRHE02-249)
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: DCT/US02/09187
PRIOR PILING DATE: 2003-03-26
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-03-14
PRIOR PILING DATE: 2002-03-14
PRIOR PILING DATE: 2002-03-14
PRIOR PILING DATE: 2002-03-14
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-02-26
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PILING DATE: 2000-02-15
PRIOR PILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PILING DATE: 2000-02-15
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GENERAL INFORMATION:
APPLICANT ROSECTE GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REPERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION OF 12002
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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100.0%; Score 12; DB 6; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 10; Conservative 2; Mismatches 0; Indels
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Pred. No. 1.4e+04;
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US-10-669-841-5016
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ORGANISM: Artificial Sequence
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CORGANISM: Homo sapiens
PCT-US02-38216-9770
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Best Local Similarity
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Sequence 78761, Application PC/TUS0238216
| SEMBRAL INFORMATION
| SEMBRAL INFORMATION
| TITLE OF INVENTION
| TITLE OF SECURITY APPLICATION
| TITLE OF SECURITY APPLICATION
| TITLE OF SECURITY APPLICATION NUMBER: PCT/US02/38216
| CURRENT APPLICATION NUMBER: PCT/US02/38216
| CURRENT FILING DATE: 2002-11-12
| SOFTWARE: Patentin version 3.2
| SOFTWARE: Patentin version 3.2
| TENDER OF SECURITY APPLICATION OF SECURITY APPLICATIO
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Sequence 72837, Application PC/TUS0238216
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REPREBRUES: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 72837
LENGTH: 21
LENGTH: 21
APPLICANT: Rosetta Genomics LTD
TTLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSQ ID NO 3: 22
SSQ ID NO 3: 329
LENGTH: 21
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Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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CRGANISM: Homo sapiens
PCT-US02-38216-78761
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; ORGANISM: Homo sapiens
PCT-US02-38216-72837
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-31329
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Best Local Similarity
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PCT-US02-38216-72837
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PCT-US02-38216-78761
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GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF PRESENCE: 55002
CURRENT APPLICANTION UNMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE? Parentin version 3.2
SEQ ID NO 78501
LENGTH: 20
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APPLICANT: ROSECTE Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 31313
LENGTH: 20
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100.0%; Score 12; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                             Query Match 100.0%; Score 12; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 1.4e+04; Matches 12; Conservative 0; Mismatches 0; Indels
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PCT-10502-38216-31329
F Sequence 31329, Application PC/TUS0238216
F GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31313, Application PC/TUS0238216 GENERAL INFORMATION:
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CORGANISM: Homo sapiens
PCT-US02-38216-78501
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; ORGANISM: Homo sapiens
PCT-US02-38216-31313
                                                                               TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-64788
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Trahes 12; Conserva
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                  SEQ ID NO 64788
                                                      LENGTH: 19
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Sequence 42141, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: ROSELTA Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICANTON NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 39287, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: ROSELTA GENOMICS LTD
APPLICANT: ROSELTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THERROF
TILE REFERENCE: 55002
CURRENT APPLICALTON NUMBER: PCT/US02/38216
CURRENT PILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 17
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Best Local Similarity 100.
Matches 11; Conservative
9 GGGTGGTGGGG 20
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CORGANISM: Homo sapiens
PCT-US02-38216-42141
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CORGANISM: Homo sapiens
PCT-US02-38216-39287
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PCT-US02-38216-39287
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PCT-US02-38216-42141
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Search completed: October 27, 2003, 18:22:56 Job time : 205.686 secs

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OM nucleic

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Run

Sequence:

Searched:

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Minimum I Maximum I

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Nucleotide sequenc
Triplex forming ol
CD28 inhibiting ol
CD28 inhibition ol
Gastric acid produ
Hammerhead ribosym
Rat PTPIB antisens
Rat PTPIB antisens
Rat PTPIB antisens
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Human POSHL1 scann
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CD28 expression in
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Hepatitis C virus
Human CC3 promocer
Triple helix formi
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Human GG0 Hammerh
Human MOGO Inozyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD28 expression inhibiting oligonucleotide, RT09s.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF05272
ABK00045
ABK00045
AAT95484
AAT95486
AAT9537997
AAC37997
AAC37997
ABK85193
ABK85193
ABK85193
ABK85193
                    AAT36197
AAX90329
AAX90291
AAF16593
AAF01954
AAD12117
ABK85192
ABK85192
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AAT98040
ABV91222
ABV91223
ABV91223
AAX56945
AAX56945
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AAX56945
AAX56945
AAX5694
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AAX14740
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95US-0529878.
95US-0387041.
95US-0529878.
    96WO-US01507
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(first entry)
    09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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    Synthetic.
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IID AAT3
AAC AAT3
AXX AAT3
DT 15-A
DT 15-A
DT 15-A
DX AXX AXX
XXX Redu
XXX Redu
XXX RW MIL-2
XXX W BSO
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| SIDSI/gcgdata/geneseq_embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq_embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq_embl/NA1982.DAT:*
| SIDSI/gcgdata/geneseq_embl/NA1982.DAT:*
| SIDSI/gcgdata/geneseq_embl/NA1983.DAT:*
| SIDSI/gcgdata/geneseq_geneseq_embl/NA1983.DAT:*
| SIDSI/gcgdata/geneseq_embl/NA1985.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn_embl/NA1990.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn_embl/NA2001B.DAT:*
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                      5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              2552756 segs, 1349719017 residues
                      version 5
- 2003 (
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Maximum Match 100%
Listing first 45 summaries
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AAX90336
AAT36242
AAT36196
AAX90328
AAX90335
AAX90290
                                                                                               nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 -
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score greater than or equal to
and is derived by analysis of t
                                                                                                                                                                                                                                               ttggagggggaggtgggg
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Match Length
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llength: 22
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AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
             method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonuclectide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                          Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; septic shock; viral disease; porriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                          .
                                                                                                                        Length 18;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                             CD28 expression inhibiting oligonucleotide, RT05s.
                                                                                                                        100.0%; Score 18; DB 20; 100.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                          Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
                                                                                                                                                          Mismatches
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                                                                                                                                                                                      1 TIGGAGGGGAGGIGGGG 18
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95US-0529878.
95US-0387041.
95US-0529878.
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                                                                                                                                                                                                                                                                                                  AAT36242 standard; DNA; 18
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(first entry)
                                                                                                                     Query Match
Best Local Similarity 100.
Matches 18, Conservative
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                                                              present invention.
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09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, postiasis, useful in the disease, postiasis, type I diabetes mellitus, thyroiditis, ascocides, multiple sclerosis, uveitis, theumatorid arthritis, systemic lupus erythematosus, inflammatory bowel disease, recting CD28 expression may reduce the effects of antigenic simulation of CD28 positive T cells, with a consequent reduction in cycokine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
                                                                             for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                     The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD28 inhibiting phosphorothioate oligonucleotide RT09S
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 18; DB 17; 100.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                        Example 2; Page 45; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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(ICNC ) ICN PHARM INC
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Best Local Similarity
Local 18; Conserve
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                                                              WPI; 1996-384228/38
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                              Tam RC;
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Matches

8 g RESULT 4 AAT36196

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonuclectide (OGN).

AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonuclectide used in the exemplification of the
                                                                                                                                                                                    CD28; inhibition; antisense oligonuclectide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.1%; Score 16.4; DB 20; Length 18; 94.4%; Pred. No. 1.40+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of immune system-mediated diseases by inhibiting of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                        CD28 inhibiting phosphorothioate oligonucleotide RT03S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD28 inhibiting phosphorothioate oligonucleotide RT05S.
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                                                     ВР.
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                                                    AAX90328 standard; DNA; 18
                                                                                                                          (first entry)
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les 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.
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                                                                                                                        24-SEP-1999
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                                                                                       AAX90328;
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                                       AAX90328
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                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                Reduction; T cell, CD28; gene expression, treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; soriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; S'-UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; S'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated disease, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, postiasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of anticenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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 Length 18;
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                                   1; Indels
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                                                                                                                                                                                                                                                                                                                Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
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Pred. No. 1.4e+03;
0; Mismatches 1;
 DB 17;
Score 16.4; DB 17
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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                                   Mismatches
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95US-0529878.
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95US-0529878.
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Best Local Similarity 94.4%;
Matches 17; Conservative
91.18;
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                                                                                                                                                                                         AAT36196 standard; DNA; 18
                                                                                                                                                                                                                                                            (updated)
(first entry)
                                   17; Conservative
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                Similarity
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09-FEB-1995;
18-SEP-1995;
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15-APR-1997
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Query Match
Best Local (
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Tam RC;

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Gaps

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The present sequence represents a G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides. The G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for tracting septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococal induced arthritis, Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection; antigen presenting cell activation; natural killer cell; septic shock; cytocoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; lyme arthritis; streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcurtaneous administration of an oligonucleotide (OGN) aAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections
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                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of G-motif oligonucleotide GR1.
                                                                                                                                                                                      Score 16.4; DB 20;
Pred. No. 1.4e+03;
0; Mismatches 1;
                                                                                                                                                Seguence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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94.4%;
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Best Local Similarity 94.45
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                                                                                                        diseases.
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AAZ99625
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                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonuclectide (OGN). AAX90298 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorothicate oligonuclectide used in the exemplification of the
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                                                                                                                                                                                                                                                                                               Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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1.4e+03;
1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
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immune system medi
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                                                                                    18-SEP-1995;
                                                                                                                            18-SEP-1995;
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    US5932556-A
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                                              03-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a non-G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides in the form of antiden presenting the digonucleotides inhibit activation of antiden presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vacines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft versus-host diseases and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chomic inflammatory bowel disease, psoriasis vulgaris, experimental allergic
                infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV)-infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-motif oligonucleotide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte, inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection; Leishmaniasis; spontaneous abortion; tumour; ss.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions comprising G-motif oligonucleotides useful for e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.
                                                                                                                                                                                                          Indels
                                                                                                                                                                Score 16.4; DB 21;
Pred. No. 1.4e+03;
0; Mismatches 1;
                                                                                                                                Sequence 18 BP, 1 A, 0 C, 13 G, 4 T, 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 14; Page 32; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CPGI-) CPG IMMUNOPHARMACEUTICALS
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                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                  91.1%;
94.4%;
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                                                                                                                                                                                                                                                                                                                                                                               AAZ99650 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                          17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-256970/22
                                                                                                                                                                                      Best Local Similarity
Matches 17; Conserv
encephalomyelitis,
                                                                                            precursor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200014217-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parasitic
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ99650;
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                             AAZ99650/c
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infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis) viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV) infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Reduction, T cell, CD28, gene expression, treatment, immune system, disorder; graft versus host disease; septic shock, viral disease; sporiasis, type I diabetes mellitus, thyroiditis; sarcoides, multiple sclerosis, uveitis; rhewmatoid arthritis; 5'-UTR, systemic lupus erythematosus, inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, e.g. graft versus host disease, septic shock, viral disease, soriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in T cells -
host disease,
                                                                                                                                                                   .
0
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uligo:nucleotide which reduces CD28 gene expression for treating immune system diseases, e.g. graft vs. septic shock, psoriasis, etc.
                                                                                                                                  Score 16.4; DB 21;
Pred. No. 1.4e+03;
0; Mismatches 1;
                                                                                                      G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 54; 77pp; English.
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95US-0529878.
95US-0387041.
95US-0529878.
                                                                                                        Seguence 18 BP; 4 A; 13 C; 0
                                                                                                                                     91.1%;
                                                                                                                                                    94.48;
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(first entry)
                                                                                                                                    Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                            AAT36197 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-384228/38
 encephalomyelitis,
                                                                            precursor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9624380-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-1996;
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15-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                          AAT36197;
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                                                                                                                                                                                                                                                                             RESULT 10
AAT36197
8899999888
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Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative

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TTGGAGGGGGGAGGTGGGG

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rredakedederecredes 21

BP.

AAX90329 standard; DNA; 21

RESULT 11

(first entry)

24-SEP-1999

AAX90329;

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                          CD28; inhibition, antisense oligonucleotide, interleukin 2, IL-2, immune system mediated disease; gamma-interferon; IL-8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gastric acid disturbance, gastric reflux, gastritis, dyspepsia, stomach ulcer, duodenal ulcer, Helicobacter pylori, antisense; DNA-RNA hybrid, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gastric acid production inhibiting oligonucleotide SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
                                                                                                                                                                                                                                                                                                                              Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4; DB 20;
Pred. No. 1.4e+03;
n. Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
CD28 inhibition oligonucleotide RT04
                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Column 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TTGGAGGGGGAGGTGGGG 18
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Best Local Similarity 94.4%;
Matches 17; Conservative
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TTGGAGGGGTGGTGGGG
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                                                                                                                                                                       95US-0529878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF16593 standard; DNA;
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                                                                                                                                                                                                                                                                                                   WPI; 1999-443609/37
                                                                                                                                                                                                                                     (TAMR/) TAM R C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200071164-A1.
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                                                                                                                                                                       18-SEP-1995;
                                                                                                                                                                                                       18-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-2000
                                                                                                           US5932556-A
                                                                                                                                          03-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF16593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases
                                                                                                                                                                                                                                                                   Tam RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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0
                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN) AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                  Gaps
                                                                                                                                                                                                                                                                                                                    IL-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
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                  Length 21;
                                                                                                                                                                                                                                                                                                        CD28; inhibition; antisense oligonucleotide; interleukin 2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                Indels
                                                                                                                                                                                                                                                                                    CD28 inhibiting phosphorothioate oligonucleotide RT04S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.4; DB 20;
Pred. No. 1.4e+03;
0; Mismatches 1;
               Score 16.4; DB 17;
Pred. No. 1.4e+03;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
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Example; Column 21; 45pp; English.

WPI; 1999-443609/37

95US-0529878

.8-SEP-1995;

JS5932556-A 03-AUG-1999

Synthetic.

95US-0529878

TAMR/) TAM R C. 18-SEP-1995;

ram RC;

78 2

TTGGAGGGGGAGGTGGGG Trecaececrecreses

91.1%; 94.4%;

Query Match
Best Local Similarity 94...
Best Local 17; Conservative

present invention.

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AAX90291 standard; DNA; 21

77

RESULT

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(first entry)

24-SEP-1999

AAX90291;

SAXEX

. 0

Gaps

. 0

Indels

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New antisense compounds capable of modulating expression of human protein phosphatase 1B, useful for diagnosis, prophylaxis and treatment of diseases associated with expression of protein phosphatase
                                                                                                                                                                                                                                                                                   Rat, PTP1B, protein phosphatase 1B inhibitor, antisense, gene thera
infection, inflammation, tumour, prophylaxis, phosphorothioate, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention is directed to antisense compounds, particularly oligonuclectides which are targetted to a DNA encoding protein phosphatase 1B (PTP1B) to modulate its expression. The antisense compounds are useful for diagnosis, prophylaxis and treatment of diseases associated with the expression of PTP1B, to prevent or delay infection, inflammation and tumour formation and as a research reagent. The PTP1B DNA is useful in gene therapy. The present sequence is an antisense oligonucleotide with a
   Length 17;
                                                                                                                                                                                                                                                      Rat PTP1B antisense oligonucleotide (ISIS# 113721)
                                                                                                                                                                                                                                                                                                                                                                                                                    /mod_base= OTHER
/note= "Phosphorothioate backbone"
   Score 14.4; DB 21;
Pred. No. 8.4e+03;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Methoxyethyl residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Methoxyethyl residues"
16..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 17; Column 51-52; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mod_base= OTHER
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93.8%;
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                                                                                                                                                                AAD12117 standard; DNA; 20
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                                                                                                                                                                                                                        (first entry)
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                                                             3 GGAGGGGGAGGTGGGG
                                                                                        16 GGAGGGGTAGGTGGGG
   Query Match
Best Local Similarity 93.8
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cowsert LM, Wyatt J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-432181/46.
                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                         Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified base
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                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                              AAD12117;
                                                                                                                                    RESULT 15
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                                                                                                                                                                                                                                                                                                  ö
                                                                                                 The present invention provides oligonucleotides, and methods for their use, which are useful in modulating the action of proteins involved in gastric acid production. The target protein is preferably the histamine H2 receptor or one of the proteins which form part of the gastric proton pump. The sequences and methods of the invention are useful in the tradement of gastric relux, gastritis, dyspepsia, stomach ulcers, duodenal ulcers and other gastric acid disturbances, most of which are caused by Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
               Treating gastric acid disturbance by administering an oligonucleotide which modulates the activity of a polypeptide involved in gastric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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0
                                                                                                                                                                                                                                                                     Length 22;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                 82.2%; Score 14.8; DB 22;
81.2%; Pred. No. 5.8e+03;
ive 3; Mismatches 0;
                                                                                                                                                                                                                                     Seguence 22 BP; 0 A; 0 C; 16 G; 3 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 2 A; 12 C; 0 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McSwiggen J;
                                                                         Example 3; Page 145; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hammerhead ribozyme substrate #249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 37; Page 61; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                AAF01954 standard; DNA; 17 BP
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                                             production or secretion
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                                                                                                                                                                                                                                                                              Local Similarity
nes 13; Conserv
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Length	2; Indels	
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Score Pred.	0, Mis	18
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Query Match 76.7%; Score 13.8; DB 22; Length 20; Best Local Similarity 88.2%; Pred. No. 1.40+04;	Matches 15; Conservative	
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Search completed: October 27, 2003, 11:25:21 Job time : 163 secs

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RESULT 2
PCT-USO2-18216-6227/C

PCT-USO2-18216-6227/C

SEQUENCE 6227, Application PC/TUSO238216

SEQUENCE 6227, Application PC/TUSO238216

SEQUENCE 6227, Application PC/TUSO238216

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGÜLATORY TITLE OF INVENTION: GENES AND USES THEREOF

CURRENT APPLICATION NUMBER: PCT/USO2/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOOTWARE: Patentin version 3.2

SEQ ID NO 6227

LENGTH: 18

TYPE: DNA

CORRENT HOMO Sapiens
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| Sequence 4726, Application PC/TUS0238216
| GENERAL INFORMATION:
| APPLICANT: Rosetta Genomics LTD
| TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
| TITLE OF INVENTION: GENES AND USES THEREOF
| TITLE REPERBNCE: 55002
| FILE REPERBNCE: 55002
| CURRENT PAPLICATION UNMBER: PCT/US02/38216
| CURRENT FILING DATE: 2002-11-12
| NUMBER OF SEQ ID NOS: 86841
| SEQ ID NO 47426
| LENGTH: 19
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PCT-USO2-38216-60884
PCT-USO2-38216-18290
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PCT-USO2-38216-39923
PCT-USO2-38216-39021
PCT-USO2-38216-39021
PCT-USO2-38216-41601
PCT-USO2-38216-41601
PCT-USO2-38216-6296
PCT-USO2-38216-52911
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larity 100.0%; Pred. No. 9.1e+03;
Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 0;
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CRGANISM: Homo sapiens
PCT-US02-38216-47426
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                     October 27, 2003, 11:09:34 ; Search time 307.029 Seconds (without alignments) 97.777 Million cell updates/sec
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'Ggn2_6/ptodata71/pna/US06_NEW_COMB.seq:*

'Ggn2_6/ptodata11/pna/US06_NEW_COMB.seq:*

'Ggn2_6/ptodata71/pna/US07_NEW_COMB.seq:*

'Ggn2_6/ptodata71/pna/US08_NEW_COMB.seq:*

'Ggn2_6/ptodata71/pna/US08_NEW_COMB.seq:*

'Ggn2_6/ptodata71/pna/US08_NEW_COMB.seq:*

'Ggn2_6/ptodata71/pna/US08_NEW_COMB.seq:*

'Ggn2_6/ptodata71/pna/US00_NEW_COMB.seq:*
                               GenCore version 5,1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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PCT-USO2_38216-68259
PCT-USO2_38216-38911
PCT-USO2_38216-38911
PCT-USO2_38216-38911
PCT-USO2_38216-38912
PCT-USO2_38216-38912
PCT-USO2_38216-126
PCT-USO2_38216-126
PCT-USO2_38216-18954
PCT-USO2_38216-18314
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PCT-USO2_38216-18278
PCT-USO2_38216-18231
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Gapop 10.0 , Gapext 1.0
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FOCT-US02-38216-6229/C
Sequence 6229, Application PC/TUS0238216
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: GENERAL SAND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT PILNG DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 6229
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39031, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Roselta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FIRE REPRESENCE: 55002
CURRENT APPLICATION VUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NORBER OF SEQ ID NOS: 86841
SOFTWARR: Patentin version 3.2
SOFTWARR: Patentin version 3.2
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) GRNERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
, TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
, TITLE OF INVENTION: BIOINFORMATICALLY
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                                                                                                  Length 17;
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93.8%; Pred. No. 1.5e+04;
tive 0; Mismatches 1;
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Pred. No. 1.5e+04;
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
  ; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38911
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CORGANISM: Homo sapiens
PCT-US02-38216-6229
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: ROSELTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SSEQ ID NOS: 86841
LENGTH: 17
                                                                                                                                    PCT-USO2-38216-18159
Sequence 18159, Application PC/TUSO238216
Sequence 18159, Application PC/TUSO238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/USO2/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 18159
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| Sequence 39032, Application PC/TUS0238216
| SEQUENCE 39032, Application PC/TUS0238216
| GENERAL INFORMATION:
| APPLICANT: ROSECTA GENOMICS LTD
| TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
| TITLE OF INVENTION: GENES AND USES THEREOF
| CURRENT APPLICANTION NUMBER: PCT/USO2/38216
| CURRENT PELING DATE: 2002-11-12
| NUMBER OF SEQ ID NOS: 86841
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 39032
| LENGTH: 16
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Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1;
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GGAGGGGAGGAGGG 17
                                              15 GGAGGGGGAGGAGGG 1
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Matches 16; Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-18159
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CORGANISM: Homo sapiens
PCT-US02-38216-39032
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Sequence 26652, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT ROSELta Genomics LTD
APPLICANT ROSELta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REPERBNCE: 55002
CURRENT PAPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOGTWAREE PACENTIN VEXEION 3.2
SEQ ID NO 26652
LENGTH: 19
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PCT-USO2-31216-6220/C
SEQUED Application PC/TUS0238216
SEQUED CE 6220, Application PC/TUS0238216
SEQUED CE 1000 Application PC/TUS0238216
SEQUED CE INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT PAPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SCOTTUARE: Patent In version 3.2
SEQ ID NO 6220
LENGTH: 17
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Sequence 38954, Application PC/TUS0238216

Sequence 38954, Application PC/TUS0238216

GENERAL INFORMATION: BCT OF INVENTION: BCT OF INVENTION: GENERAL TITLE OF INVENTION: GENERAL PERSON

CURRENT PILLE DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2
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Pred. No. 2.1e+04;
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Best Local Similarity 100.0%; Pr
Matches 14; Conservative 0;
        3 GGAGGGGGAGGAGGGG 18
                                                     17 GGAGGGGGAGGAG 2
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; ORGANISM: Homo sapiens
PCT-US02-38216-38954
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CORGANISM: Homo sapiens
PCT-US02-38216-6220
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT Rosetta Genomics LTD
APPLICANT Rosetta Genomics LTD
APPLICANT ROSETTA
APPLICANT ROSETTA
APPLICANT ROSETTA
APPLICANT ROSETTA
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 5502
CURRENT APPLICALION NUMBER: PCT/US02/38216
CURRENT APPLICALION NUMBER: PCT/US02/38216
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 19
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PCT-USO311936A-126/c
| Sequence 126, Application PC/TUS0311936A
| GENERAL INFORMATION:
| APPLICANT: Crea, Roberto:
| TILLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
| PILE REFERENCE: 1551.2001003
| CURRENT FILING DATE: 2003-04-16
| PRIOR APPLICATION NUMBER: 60/373,558
| PRIOR FLING DATE: 2002-04-16
| PRIOR FLING DATE: 2002-04-17
| NUMBER OF SEQ ID NOS: 423
| SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                   Query Match 80.0%; Score 14.4, DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 1.5e+04; Matches 15; Conservative 0; Mismatches 1; Indels
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        GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/USO2/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86941
SSCTWARE: Patentin version 3.2
EEQ ID NO 41647
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Best Local Similarity 93.8<sup>1</sup>
Matches 15, Conservative
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, ORGANISM: Homo sapiens
PCT-US02-38216-41647
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; ORGANISM: Homo sapiens
PCT-US02-38216-38912
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Sequence 14763, Application PC/TUS0238216
Sequence 14763, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
FILE REFERENCE: 55002
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFFWARE: Patentin version 3.2
ERQ ID NO 14763
LENGTH: 18
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PCT-USO2-38216-18314

PCT-USO2-38216

SERVEDATION: BOBLICATION PC/TUSO238216

GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/USO2/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

SOFTWARE: DATE OF 13.2

STYPE: DNA
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76.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                          Query Match 77.8%; Score 14; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 2e+04; Matches 14; Conservative 0; Mismatches 0; Indels
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CORGANISM: Homo sapiens
PCT-US02-38216-14763
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PCT-US02-38216-18314
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26652
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PCT-US02-38216-14763
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AZ579189 IM0363112 AZ775540 AZ775540 IM0363113 AZ775540 IM03561118 AZ64526 IM0357118 AZ64526 IM0537620 AZ65575 IM0537620 AZ657707 IM0583118 AZ65116 IM0637620 AZ77707 IM0583118 AZ7707 IM0583118 AZ751146 IM064202 AZ776115 ZM0184813 AZ68408 IM0378023 AZ6871715 ZM0184813 AZ6871715 ZM0184813 AZ6871715 ZM0184813 AZ677246 IM0662811 AZ871708 ZM0184813 AZ677246 IM0662013 AZ677246 IM06729018 AZ677246 IM06729018 AZ677246 IM06729018 AZ677246 IM06729018 AZ677246 IM06729018 AZ677246 IM06729018 AZ666896 IM06729024 AZ666896 IM0676965 AZ666896 IM066805 AZ666896 IM066805 AZ666896 IM066805 AZ666896 IM066805 AZ666896 IM066806 AZ666896 IM066806 AZ666896 IM066806 AZ666896 IM066806 AZ666896 IM066806 AZ666896 IM066806 AZ666896 IM068906 AZ666996 IM068906 AZ666896 IM068906 AZ666896 IM068906 AZ666896 IM068906

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A1251781
qu76g01.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032 3'
similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN ', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryogista, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarxhini, Hominidae, Homo. I (bases 1 to 19)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute / National Institute of Neurological Josedese and Stroke, Brain Tumor Genome Anatomy Project Unpublished
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Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 19
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AZ387199
AZ967090
AA911600
A1568336
AZ766712
                                              AZ760597
AZ775540
AZ783420
AZ512326
AZ645269
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AZ772707
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A1251781.1 GI:3848310
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Homo sapiens
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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A2876923 2M0192D07
AU254493 AU254493
A1582080 ar96b07.x
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(without alignments)
276.576 Million cell updates/sec
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5.1.6
Compugen Ltd.
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 GenCore version
Copyright (c) 1993 - 2003
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28 AZ876923
9 AU254493
9 AI582080
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length: 22
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AZ579495 1M0367C13 A1434548 ti49d05.x A1735392 at10e10.x BQ585098 E011826-0

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was blunt end-repaired with T4 DNA polymerase and T4 daptor oligomed secres. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4712114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 bp mRNA linear EST 25-APR-2002
AU254493 3'-directed mouse cDNA library Mus musculus cDNA clone
BEDD002246 3', mRNA sequence.
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Kato, K. and Matoba, R. Generation of expressed sequence tags from mouse brain
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.7%; Score 13.8; DB 28; Length 22; Best Local Similarity 88.2%; Pred. No. 4.8e+05; Matches 15; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mrna"
/db_xref="taxon:10090"
/clone="BED000246"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kikuya Kato
Graduate School of Biological Sciences
Graduate School of Science and Technology
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp,
Location/Qualifiers
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Pred. No. 6.3e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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Mus musculus
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Best Local Similarity 93.3
Matches 14, Conservative
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A1582080/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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JOURNAL
COMMENT
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AU254493
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                       /mol_type="mRNA"
/db_xref="taxon:9606"
/dlone="lwAGE:1978012"
/tissue_type="tumor, 5 pooled (see description)"
/tissue_type="tumor, 5 pooled (see description)"
/lab.host="blub="tumor, 5 pooled (see description)"
/lab.host="lub="tumor, 64P Brn3s"
/dlone lib="Nori CGAP Brn3s"
/dlone lib="nori CaAP Brn3s"
/dlone lib="nori CaAP Brn3s"
/dlone lib="tumor, 7 cloned unidirectionally, Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
1 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ876923 22 bp DNA linear GSS 21-FEB-2001 SM0192D07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0192D07 F, genomic survey sequence. AZ876923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toase; 1 to 2)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Insert Length: 10000 Std Error: 0.00
Plate: 0192 row: D column: 07
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0192D07"
       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 22.
Location/Qualifiers
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Mus musculus
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Best Local Similarity 88.2
Matches 15; Conservative
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Fax: 801 585 7177
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84112, USA
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AZ876923
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DEFINITION
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| 1.16 |
| / organism== Homo sapiens" |
| / organism== Homos |
| organism==
                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: gapbs.remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Bunnert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Bequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINN at:

www-bio.llnl.gov/bbrp/image/image.html
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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      1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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100.0%; Pred. No. 8.5e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality Insert Length: 514 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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Mus musculus
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100.0%; Fre
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AZ345792.1 GI:10425029
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                                                                                               Tumor Gene Index
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Unpublished
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Best Local Similarity
Matches 13; Conserv
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AZ345792
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16 bp mRNA linear EST 27-AUG-1998 or69hil.si NCI CGAP_GC3 Home sapients cDNA clone IMAGE:1661157 3's similar to SW:PRPE HUMAN POSBIL BASIC PROLINE-RICH PEPTIDE P-E contains element MSR1 repetitive element i, mRNA sequence.
                                                                                                                                                                                                                             Eukaryogis, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Hobses, 1 to 23.
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moche, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Washte, Y., Wyle, T., Waterston, R. and Wilson, R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
Trace considered oversall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.4; DB 9; Length 2
Pred. No. 6.3e+05;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2173429"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 מ
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                                                                                         AI582080.1 GI:4567977
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87.5%;
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                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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AA968729
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                                                                                         ACCESSION
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source

FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orfifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-complement. Soli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 19)
10 (bases 1 to 19)
11 (bases 1 to 19)
12 (ann.) Anoyaci, Manhoud, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10Xb plasmid UUGCIM library"
/nore="Vector: pWb42ny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
   S. 2030 E., SLC,
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Rm. 308, Biomedical Polymers Research Bldg., 20
                      84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0244 row: H column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
                                                                                                                                                                                                   Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/clone="UUGC1M0244H23"
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Contact: Robert B. Weiss
University of Utah Genome Center
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AZ579189/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymurclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (914732114) [ab] APL29072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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/clone lib="Mouse l0kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C37BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 12
Seq primer: CACAAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0080G12"
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Best Local Similarity 87.5
Matches 14; Conservative
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RESULT 7 AZ447248/c LOCUS ORGANISM

SOURCE

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

BASE COUNT ORIGIN

0

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/Bab host="E" Coli strain XLID-Gold, Th-resistant, F""
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/clone_lib="Wouse 10kb plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor olignmucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gence from a derivative
of pMD42 (gi|q132114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XILO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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AZ775540
GSS.
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Mus musculus
Mus musculus
Mus musculus

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: N column: 21
Seq primer: GGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554N21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Jab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/ Jab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/ Clone lib="Mouse 10kb plasmid UUGGIM library"
/ Lote="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/ Chitch for Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (4)14722141(4)26/PAT22072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the innert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored for ampicillin resistance."

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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse, Whole genome scaffolding with paired end reads from 10kb
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        University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                        Rm. 308, Biomedical Polymers Research Bld 84112, USA
Tel: 801 585 5606
Fax: 801 585 5177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: I column: 12
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0363112"
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Location/Qualifiers
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Contact: Robert B. Weiss
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gplAH22072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicallin resistance."
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1M0357118R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0357118 R, genomic survey sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longaore,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G78BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                 20 S. 2030 E., SLC,
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Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
84112, USA
                                                                                                                                                                                                        Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
llsert Length: 10000 Std Error: 0.00
Plate: 0025 row: D column: 07
Seq primer: CGTIGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"

mol_type="genomic DNA"

strain="c57BL/6"

/db xref="taxon:10090"

/clone="UUGC2M0025D07"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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Best Local Similarity 87.5%
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(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis, Vector DNA was prepared from a derivative
of pMD42 (gi|4712114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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AZ783420 GI:12918130
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Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G518L/6J (male) was obtained from the Jackson
                                                                                                                  S. 2030 E., SLC,
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   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                     Tel: 801 585 5606 Fax: 801 585 7177 Tel: 801 585 7177 Tel: 801 585 7177 Tel: 801 585 7187 Tel: 801 8 Tel: 801 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="c57BL/60"
/db xref="taxon:10090"
/clone="UUGC2M0008H15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 19.
Location/Qualifiers
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Laboratory Mouse Divide the Control Libraria, 1201 (1982). March Laboratory Mouse Divide the Control Laboratory Mouse Divide the Control Laboratory Mouse Divide the Constant velocity. The Sheared Divide My repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polywincleotide kinase. Adaptor oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarces gel electrophoresis. Vector DNA was prepared from a derivative of pWH42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptors and selected for analysically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0537F22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0537F22 F, genomic survey sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases, 1 to 20)
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                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/lab_host="E. Coli strain Xbl0-Gold, Tl-resistant, F-"
     Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 9.7e+05;
0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seg primer: CACACAGBAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                      plasmid inserts
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1M0510B10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0510B10 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                             SLC,
plasmid inserts

Unbublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

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71.1%; Score 12.8; DB 28; Length 20;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                         Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel. electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="E. Coli strain XLIO-Gold, TI-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/60 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Emsert Length: 10000 Std Error: 0.00
Plate: 0583 row: L column: 18
Seg primer: CACACAGGAAACAGCTATGACC
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Figh quality sequence stop: 20.
Location/Qualifiers
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/strain="CS7BL/6J"
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MOS83L18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIMO583L18 R, genomic survey sequence.
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Dunn, D., Aoyag, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
| note="Vector: PWD42nv; Purified genomic DNA from M. musculus G78EL/6U (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                              Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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llarity 87.5%; Pred. No. 9.75+05;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                            Rm. 308, Biomedical Polymers Research Bld. 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Ext Extrar: 0.00 Flate: 0537 zow: F column: 22 Seq primer: GGTTGTAAAACGACGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0537F22"
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   and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GGAGGGGGAGGAGGGG 18
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les 14; Conserv
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Best Local S:
Matches 14
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
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AUTHORS
                                                                                     JOURNAL
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                              TITLE
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Sequence 2, Sequen Sequence 38 Patent No. 53

Sequence 38, 7 Sequence 38, 7 Sequence 38, 7

Seguence

Sequence

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Sequence 45, Application US/09092077

Sequence 45, Application US/09092077

Patent No. 6194142

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moncany, Maurice
APPLICANT: MIVENTION: Mancany, Mancanter of The HIV-1, HIV-2 And SIV Type,
TITLE OF INVENTION: Genome Of These Retroviruses And For The In Vitro Diagnosis
TITLE OF INVENTION: Of The Diseases Due To Those Viruses
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,077
FILING DATE:
US-08-396-851A-54
US-08-491-334A-51
US-08-491-334A-54
US-08-09-027-4449-38
US-08-09-026-98-38
US-09-121-952A-38
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US-08-486-88-2
US-08-486-88-2
US-08-486-813-3
US-08-486-813-3
US-08-486-913-3
US-08-486-913-3
US-08-486-913-3
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US-08-486-913-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 05,146
REPERENCE POCKET NUMBER: 02356.0062-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Dunner
: 1300 I Street, N.W., Suite 700
Washington
                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/472,928
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/160,465
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNDRER: FR 8912371
FILING DATE: 20-SEP-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
ATTORNEY/AGENT INFORMATION:
                            (202)408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
     US-09-092-077-45
   COUNTRY:
     0000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45, Applisequence 4, Applisequence 4, Applisequence 45, Applisequence 127, Applisequence 93, Applisequence 26, 
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282, App
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69, Appl
70, Appl
83, Appl
63, Appl
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Sequence 5, A
Sequence 51,
Sequence 54,
Sequence 54,
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Sequence 59
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  5.1.6
Compugen Ltd.
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US-08-529-878B-4
US-08-529-878B-4
US-08-173-489C-127
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US-09-661-123-30
US-09-491-123-30
US-09-491-123-30
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US-09-491-123-30
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US-09-491-123-30
US-08-863-639A-51
US-08-863-639A-53
US-08-398-613A-54
US-08-398-613A-54
US-08-398-613A-54
US-08-398-611A-54
US-08-398-611A-54
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                    version 5
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
                    GenCore (c) 1993
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score greater than or equal to
and is derived by analysis of
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                                     Copyright
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length: 22
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Match
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Maximum DB
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Length 18;
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NUMBER OF SEQUENCES:

ADDRESSED: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Crockett & Fish STREET: 3000 S. Augusta Court
CITY: La Habra
COUNTRY: United States of America
CONTRY: United States of America
CONTRY: United States of America
CONTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: 13 MPC COMPATIBLE
COMPUTER: 13 MPC COMPATIBLE
CONTREMI APPLICATION NUMBER: US/08/529,878
FILING DATE: 13-521-1995
CLASSIFICATION NUMBER: 213/003
TELECOMMUNICATION NUMBER: 213/003
TELEFRAX: 714-525-3303
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: METHODS AND
NUMBER OF SEQUENCES: 48
COMPRESSORDENCES: 48
CONFEST: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
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88.9%; Pred. No. 8.2e+02;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Worderfect 6.1
CURRENT APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: Fish, Robert D:
REGISTRATION NUMBER: 33,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %2-08-529-878B-4; Sequence 4, Application US/08529878B; Patent No. 5923556; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTGGAGGGGAGGAGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
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Best Local Similarity
Matches 16; Conserve
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                                                                                                                                                                                                                                 Query Match 85.6%; Score 15.4; DB 3; Length 21; Best Local Similarity 94.1%; Pred. No. 4.8e+02; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08529878B
Patent No. 593256
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSE: Crockett & Fish STREET: Dander of America STREET: Dander of America STREET: United States of America STREET: United States of America STREET: United States of America COUNTRY: United States of America STREET: WordPerfect 6.1
COMPUTER READABLE FORM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1
COMPUTER: NordPerfect 6.1
COMPUTER: NordPerfect 6.1
CURRENT APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D: REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELEPROMUNICATION INFORMATION:
THE TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
THE TELEPROMUNICATION INFORMATION:
THE TEL
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APPLICANT: Tam, Robert C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTGGAGGGGGAGGAGGGG 18
                                                                                  . . .vroLoGY: linear . . . . . MoLECULE TYPE: DNA (genomic) US-09-092-077-45
                                                                                                                                                                                                                                                                                                                                                                2 TGGAGGGGGAGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TGGAGGGGGAGGAG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: unknown
             21 base pairs
                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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US-08-529-878B-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-08-529-878B-3
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                                          US-08-173-489C-127/C

Sequence 127, Application US/08173489C

Sequence 127, Application US/08173489C

Sequence 127, Application US/08173489C

SEGUENCE SEGUENCE

APPLICANT: WANG, C. -G.

STREET: 510 EAST 73RD STREET,

STATE: NEW YORK

STATE: NEW YORK

STATE: NEW YORK

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The 3' untranslated regions of the duplicated human alpha-globin genes are unexpectedly divergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE: 1980
RELEVANT RESIDUES IN SEQ ID NO: 127 :FROM 1 TO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: alpha-1-globin gene (accession
DESCRIPTION: V00491) nucleotides 827 to 843
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 12 inch, 1.44Mb storage
COMPUTER: 12 inch, 1.44Mb storage
COMPUTER: 12 inch, 1.44Mb storage
SOFTWARE: Wordperfect Version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 2 OCT 1992
ATTORNEY AGENT INFORMATION:
NAME: Handelman, JOSEPH H.
REGISTRATION NUMBER: 26.179
REFERNEY/DOCKET NUMBER: 26.179
REFERNEY/DOCKET NUMBER: US518-6
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (ALLORINGY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
PUBLICALISM: Home sapiens
PUBLICATION INFORMATION:
AUTHORS: Michelson, A M, Orkin, S H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ud-188
212) 246-8959
127:
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(212) 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (attorney) (21 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
--hea 15; Conserve
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US-09-780-173A-93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL:
VOLUME: 2
PAGES: 37
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Pred. No. 8.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                 Score 14.8; DB 2; Length 21;
Pred. No. 8.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/08529878B
Sequence 45, Application US/08529878B
Sequence 45, Application US/08529878B
Sequence 45, Application US/08529878B
Patent No. 592556
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
COMPRESSED Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STREET: 4000 S. Augusta Court
COUNTRY: United States of America
STREET: Galifornia
COUNTRY: United States of America
SIP: 90631
COMPUTER READABLE FORM: PC-DOS/MS-DOS
SOFTWARE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MOXIGNETECT: USPELICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION NUMBER: 33,880
REGISTRATION NUMBER: 33,880
REGISTRATION NUMBER: 33,880
REGISTRATION NUMBER: 33,880
RESERRENCE/DOCKET NUMBER: 213/003
TELEPHONE: 714-525-3303
TELEPRAX: 714-525-3303
REFERENCE/DOCKET NUMBER: 213/003
TELECOMNUICATION INFORMATION:
TELEPHONE: 714-525-3333
TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTGGAGGGGGAGGAGGGG 18
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                                                                                                                                                                                                                                  ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%;
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                         TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-529-878B-45
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US-09-495-140-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brenda F. Baker
APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION
FILE REPRENCE: TS-0063
CURRENT APPLICATION NUMBER: US/09/344,579
CURRENT APPLICATION NUMBER: 1999-06-25
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nichais M. Dean
APPLICANT: Nichais M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REPERENCE TITLO NUMBER: US/09/490,692
CURRENT APPLICATION NUMBER: US/09/490,692
NUMBER OF SEQ ID NOS: 176
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                             Query Match 71.1%; Score 12.8; DB 4; Best Local Similarity 87.5%; Pred. No. 4.7e+03; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Antisense Oligonucleotide US-09-490-692-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
EARLIER APPLICATION NUMBER: 09/389,566
EARLIER FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: 08/856,141
EARLIER FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 153, Application US/09490692; Patent No. 6180353; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09344579
Patent No. 6054316
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGAGGGGGAGGAGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GGAGGGGAGGAGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Seguence
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGAGCGGGAGGAGGAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 87.5
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-490-692-153/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-344-579-9
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                                         GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
FILE REPREBRUCE: RTS-0165
CURRENT APPLICATION NUMBER: US/09/780,173A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT
TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION
FILE REFERENCE: 19113.0081
CURRENT APPLICATION NUMBER: US/09/495,140
CURRENT FILING DATE: 2000-01-31
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APPLICANT: Susan F. Murray
TITLE OF INVENTION ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
FILE REPERENCE: 1SSH-0498
CURRENT APPLICATION NUMBER: US/09/661,753
CURRENT FILING DATE: 2000-099.14
EARLIER PELING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 30
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          76.7%; Score 13.8; DB 4; Length 20; 88.2%; Pred. No. 2e+03; cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.4%; Score 13.4; DB 4; Length 20; 93.3%; Pred, No. 2.8e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Antisense Oligonucleotide US-09-780-173A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-09-661-753-30
    Sequence 93, Application US/09780173A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-495-140-26
Sequence 26, Application US/09495140
Patent No. 6376182
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-661-753-30/c
; Sequence 30, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGGAGGAGGAG 18
                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Seguence
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APPLICANT: CHAO, JULIE
APPLICANT: SONG, QING
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 14; Conserv
                                                                                                                                                                                                                                                       SEQ ID NO 93
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                               FEATURE:
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Matches
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                                                                                                                                                                                                                                                                               COUNTRY: USA.

ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel Worderfect 8 version
SOFTWARE: Corel Worderfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILICA DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 11859-1
TELEPHONE: (626) 795-6410
TELEPHONE: (626) 795-6421
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-863-639A-53/C
; Sequence 53, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Rampal, Jang B.
TITLE OF THATION OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                        APPLICANT: Matson, Robert S.
APPLICANT: Cassain, Peter J.
APPLICANT: Cassain, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSE: Sheldon & Max
STREET: 225 South Lake Avenue, 9th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: Windows 95 SOFTWARE: COTE! WordPerfect 8 version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/863,639A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.8; DB 2;
Pred. No. 4.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 South Lake Avenue, 9th Floor CITY: Pasadena STATE: CA COUNTRY: USA ZIP: 91101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                      STATE: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                         APPLICANT: Prockop, Darwin J.
APPLICANT: Prockop, Darwin J.
APPLICANT: Prockop, Darwin J.
APPLICANT: Milliams, Charlene J.
APPLICANT: Williams, Charlene J.
APPLICANT: Rivaniemi, Pertti
APPLICANT: Raldwin, Clinton
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
APPLICANT: Hopkinson, Ian
TITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:
ADDRESSED: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·
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71.1%; Score 12.8; DB 3; Length 20; 87.5%; Pred. No. 4.7e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTAIN COLD AND COMPUTER READABLE FORM:
MEDIUM TYPE: 10 DISKETTE, 3.5 INCH
COMPUTER: 12 DM COMPATIBLE, 3.5 INCH
COMPUTER: 12 DM COMPATIBLE
COMPUTER: WINDAWS 3.1
SOFTWARE: WORDERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
RECORDERATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 12-NOV-1993
PRIOR APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mark DeLuca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1082
TELECOMMUNICATION INFORMATION:
TELECHOMNICATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1082
TELECOMMUNICATION NUMBER: 33,239
REFERENCE (215) 568-3439
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           US-08-256-426B-282/c
; Sequence 282, Application US/08256426B
; Patent No. 5948611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41, Application US/08863639A Patent No. 5981185
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Best Local Similarity 87.5%;
Matches 14; Conservative (
                                                                                          3 GGAGGGGGAGGGGG 18
                                                                                                                                      16 GGAGGAGGAGGAG 1
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                     Best Local Similarity 87.5
Matches 14; Conservative
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TOPOLOGY: LINEAR
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US-08-256-426B-282
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US-08-863-639A-41
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  Query Match
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Search completed: October 27, 2003, 14:03:35 Job time : 42.3143 secs

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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER READBABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION NUMBER: 20,532
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Muehr
REFERENCE/DOCKET NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELEPHONE: (626) 796-400
TELEPHONE: (626) 796-400
TELEPHONE: (626) 796-400
TELEPHONE: (626) 796-6321
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Cassin, Peter J.
APPLICANT: Cassin, Peter J.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS NUMBER OF SEQUENCES: 95
CORRESPONDENCE: 95
ADDRESSEE: Shaldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
71.1%; Score 12.8; DB 2;
Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2;
CLASSIFICATION: 435

TURNEY/AGRY INFORMATION:
NAME: JOSEPh E. Much
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELEPHONE: (626) 795-6321
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDENDESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-08-863-639A-59/c
Sequence 59, Application US/08863639A
Patent No. 5981185
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CITY: Pasadena
STATE: CA
COUNTRY: USA
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26, Appl 11, Appl 4054, Ap 153, App

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Sequence 10, Appl Sequence 38, Appl Sequence 866, Appl Sequence 866, Appl Sequence 866, Appl Sequence 174, Appl Sequence 1939, Appl Sequence 1939, Appl Sequence 26, Appl Sequence 893, Appl Sequence 893, Appl Sequence 1833, Appl Sequence 161, Appl Sequence
                                                                              Sequence 11.
Sequence 15.
Sequence 15.
Sequence 9, 4.
Sequence 10.
Sequence 10.
Sequence 902.
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2 US-10-059-877-26
1 US-10-303-109A-30
1 US-10-303-109A-30
1 US-10-303-109A-30
2 US-10-109-868-11
2 US-10-12-585-4054
4 US-10-181-846-153
4 US-09-88-034-9
1 US-09-726-258-38
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APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN I
FILE REPERBENCE: P80.78
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%; Score 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1934, Application US/10061201 Publication No. US20030166229A1 GENERAL INFORMATION:
          ORGANISM: Homo sapiens
US-10-061-201-1934
     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                           ; Search time 387.943 Seconds (without alignments) 124.432 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NBW_PUBLseq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NBW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_NBW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO6_NBW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-061-201-1935
US-09-828-034-28
US-10-061-201-1937
US-10-061-201-1937
US-09-948-002-30
US-09-948-002-30
US-09-780-533A-46
US-09-780-533A-901
US-09-780-533A-901
US-10-061-201-1938
US-10-061-201-1938
US-09-780-533A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1792395 seqs, 1340900451 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                          nucleic search, using sw model
                                                                                                                                                                        October 27, 2003, 11:25:34
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Gapop 10.0 , Gapext 1.0
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18
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length: 22
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Match
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Perfect score:
Sequence:
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Maximum DB seq
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83.3%; Score 15; DB 12; I
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0;
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88.9%; Pred. No. 6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09828034
GENERAL INFORMATION:
APPLICANT: Zhong, Weidong
APPLICANT: Hong, Zhi
APPLICANT: Ferrari, Eric
TITLE OF INVENTION: HCV REPLICASE COMPLEXES
FILE REPRENCE: INDIGS
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
FRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1933, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICATE SHARMON, MATK
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
PILE REPERBNCE: P80178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
  PRICR APPLICATION NUMBER: PCT/USO1/00665
PRICR FILING DATE: 2001-01-30
PRICR PLICATION NUMBER: PCT/USO1/00668
PRICR PLING DATE: 2001-01-30
PRICR PLING DATE: 2001-01-30
PRICR PELING DATE: 2001-01-30
PRICR PELING DATE: 2001-01-30
PRICR FILING DATE: 2001-01-30
PRICR PLICATION NUMBER: PCT/USO1/00670
PRICR PLICATION NUMBER: US 09/864,761
PRICR PLICATION NUMBER: US 06/328,205
PRICR PLING DATE: 2001-05-23
PRICR PLING DATE: 2001-05-23
PRICR PLING DATE: 2001-05-30
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GAGGGGGAGGAGGGG 18
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Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-061-201-1936
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US-10-061-201-1933/c
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                           Indels
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0;
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Sequence 1936, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORWATION:
APPLICANT: Shannon, Mark
ITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REPERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT PILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                Sequence 1935, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
                                                             4 GAGGGGGAGGAGGGG 18
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Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                 RESULT 2
US-10-061-201-1935/c
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Sequence 46, Application US/09780533A

Sequence 46, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Haeberli, Fete

TITLE OF INVENTION Method and Reagent for the Inhibition of NOGO Gene

TITLE OF INVENTION Method and Reagent for the Inhibition of NOGO Gene

CURRENT APPLICATION NUMBER: US/09/780,533A

CURRENT PELICATION NUMBER: US 60/181,797

PRIOR FILING DATE: 2000-02-11
                                                                                                                                                          Gaps
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US-09-948-002-30/c
US-09-948-002-30/c
US-09-948-002-30/c
US-09-948-002-30/c
US-09-948-002-30/c
US-09-948-002-30/c
US-09-948-002-30/c
US-09-948-002
US-09-948-003

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                                                                      Length 17;
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                                                                                                                1.3e+04;
                                                                 Score 14; DB 12;
Pred. No. 1.3e+04
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                                     77.8%; SCC-
100.0%; Pre
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGAGGGGGAGGAGGG 17
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Best Local Similarity 100.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                  14 GAGGGGGAGGAGGG 1
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                                                                      Query Match
Best Local Similarity 100.
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-780-533A-46
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US-09-780-533A-46/c
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PUBLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN I
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT APPLICATION NUMBER: US/10/066,201
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
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PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
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LENGTH: 17
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; ORGANISM: Homo sapiens
US-10-061-201-1937
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US-10-061-201-1933
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NS-09-780-533A-901/c

| Sequence 901, Application US/09780533A |
| Publication No. US20030060611A1 |
| Publication No. US20030060611A1 |
| GENERAL INFORMATION: |
| APPLICANT: Ribozywe Pharmaceuticals, Inc. |
| APPLICANT: Blatt, Larry |
| APPLICANT: Haberli, Pet and Reagent for the Inhibition of NOGO Gene |
| TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene |
| FILE REFERENCE: MEHBOO, 878-A (400/01) |
| CURRENT FILING DATE: 2001-02-09 |
| PRIOR APPLICATION NUMBER: US 60/181,797 |
| PRIOR APPLICATION NUMBER: US 60/181,797 |
| SOFFWARE: Patentin version 3.0 |
| SOFFWARE: Patentin version 3.0 |
| SEQID NO 901
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Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN FOSH-LIKE PROTEIN 1
FILE REPERENCE: PROTEIN 1
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
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          Publication No. US20030060611A1
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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TYPE: RNA
CRGANISM: Homo sapiens
US-09-780-533A-901
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ORGANISM: Homo sapiens
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                                                                                                      US-09-780-533A-47/C

US-09-780-533A-47/C

Sequence 47, Application US/09780533A

Publication No. US-20030060611A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowrita, Blact, Larry
APPLICANT: Chowrita, Bharat
APPLICANT: McSwiggen, Jim
APPLICANT: McMarat
APPLICANT: APABER (1)
APPLICANT: McMarat
APPLICANT
APP
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US-09-780-533A-899/c
is Sequence 899, Application US/09780533A
is Publication No. US20030660611A1
is GENERAL INFORMATION:
is APPLICANT Ribozyme Pharmaceuticals, Inc.
is APPLICANT: Blatt, Larry
is APPLICANT: McSwiggen, Jim
is APPLICANT: Haeberli, Pete
is TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
is FILE REPRENCE: MBHB00, 878-A (400/011)
is CURRENT FILING DATE: 2001-02-09
is PRIOR APPLICATION NUMBER: US 60/181,797
is NUMBER OF SEQ ID NOS: 6679
is SOFTWARE: PatentIn version 3.0
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Pred. No. 3e+04;
0; Mismatches 0; Indels
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72.2%; Scr
Best Local Similarity 100.0%; Pr
Matches 13; Conservative 0;
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16 GGGGAGGAGGGG
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CRGANISM: Homo sapiens
US-09-780-533A-899
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; ORGANISM: Homo sapiens
US-09-780-533A-47
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RESULT 11 US-09-780-533A-900/c ; Sequence 900, Application US/09780533A

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Sequence 45, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION

APPLICANT: Ribozyme Plarmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Howaring, Pete

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

TITLE REPERENCE: MEMBOO, 9780, 533A

CURRENT APPLICATION NUMBER: US/09/780, 533A

CURRENT APPLICATION NUMBER: US 60/181, 797

PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 6679

SEQ ID NOS: 6679

LENGTH: 17

LENGTH: 17
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Pred. No. 3.6e+04;
0; Mismatches 2;
                                                                                 DB 12;
                                                                                     Query Match 72.2%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 3e+Matches 13; Conservative 0; Mismatches
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Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                                                                                                                                                                     4 GAGGGGGAGGG 16
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CRGANISM: Homo sapiens
US-09-780-533A-45
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US-09-780-533A-45/c
                     US-10-061-201-1938
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Pred. No. 3e+04;
0; Mismatches 0; Indels
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TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PRO178
CURRENT APPLICATION NUMBER: US/10/61,201
CURRENT FILING DATE: 2002-01-30
FRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/664,761
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PLICATION NUMBER: US 09/664,761
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: USO1-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1932
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Publication No. US20030166229A1
GENERAL INFORMATION:
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72.2%; Soc
Best Local Similarity 100.0%; Pr
Matches 13; Conservative 0;
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; ORGANISM: Homo sapiens
US-10-061-201-1932
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ORGANISM: Homo sapiens
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US-10-061-201-1938/c
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(SGDZ 6 Prodata/Ipna/PCTUS COMB.Seq:*

(SGDZ 6 Prodata/Ipna/BCTUS COMB.Seq:*

(SGDZ 6 Prodata/Ipna/USOB CO
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33363688 seqs, 16581889874 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                 ttggagggggaggggg 18
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18
1 ttggaggggaggag
                             Copyright
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Perfect score:
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cgn2_6/ptodata1/pna/US100B_COMB.seq:
cgn2_6/ptodata1/pna/US101B_COMB.seq:
cgn2_6/ptodata1/pna/US101B_COMB.seq:
cgn2_6/ptodata1/pna/US101B_COMB.seq:
cgn2_6/ptodata1/pna/US101B_COMB.seq:
cgn2_6/ptodata1/pna/US101B_COMB.seq:
cgn2_6/ptodata1/pna/US6001_COMB.seq:
cgn2_6/ptod
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1/pna/US6021_COMB.seq:*
1/pna/US6022_COMB.seq:*
1/pna/US6023A_COMB.seq:*
1/pna/US6023A_COMB.seq:*
1/pna/US6024_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 7, Appli Sequence 4, Appli Sequence 47426, A Sequence 5, Appli
σι	18 100.0 18 19 US-09-331-204A-7 18 100.0 19 19 US-09-331-204-4 17 94.4 19 50 US-10-310-188-47426 16.4 91.1 18 19 US-09-331-204-5
DB	4 4 5 4 6 6 6 6 6
* Query Match Length DB	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
* Query Match	18 100.0 18 100.0 17 94.4 16.4 91.1
Score	18 18 17 16.4
esult No.	H 0 W 4

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Sequence 47426 Application US/10310188

SEGUENCE 47426 Application US/10310188

GENERAL INFORMATION:
APPLICANT: ROSettaGemonics
APPLICANT: ROSettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTION: UNDER: 07/10/310,188
CURRENT APPLICATION UNDER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 47426
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                                                                                                                                                                                  APPLICANT: Tam, Robert

APPLICANT: Tam, Robert

ITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN

ITLE OF INVENTION: IMMUNE RESPONSE

FILE REFERENCE: ICNSequence

CURRENT APPLICATION NUMBER: US/09/331,204

CURRENT APPLICATION NUMBER: US/09/331,204

PRIOR FILING DATE: 1997-12-19

PRIOR FILING DATE: 1997-12-19

WIMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 19
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1. Sequence 5, Application US/09331204

1. Sequence 5, Application US/09331204

1. Sequence 5, Application US/09331204

1. Sequence 6, Application US/09331204

1. TITLE OF INVENTION: IMMUNE RESPONSE

1. TITLE OF INVENTION: IMMUNE RESPONSE

2. TITLE OF INVENTION: INVENTION: US/09/331,204

3. CURRENT APPLICATION UMBER: 1999-08-20

3. CURRENT FILING DATE: 1999-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: An oligomer OTHER INFORMATION: or polymer of ribonucleic acid or decxyribonucleic OTHER INFORMATION: acid. This term includes oligomers consisting of OTHER INFORMATION: naturally occurring bases, sugars and interesigar (
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US-09331-204-4
Sequence 4, Application US/09331204
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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Matches 17; Conserv
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tam, Robert
APPLICANT: 1897-12-19
APPLICANT: FILING DATE: 1997-12-19
APPLICANT: Patentin Version 3.0
APPLICANT: Batter APPLICANT: APPLICANT:
                                          Sequence 45, Appl
Sequence 193, Appl
Sequence 1935, Ap
Sequence 1936, Ap
Sequence 1894, Ap
Sequence 16894, Ap
Sequence 17, Appli
Sequence 17, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 67, Appli
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Sequence 28,
Sequence 181
Sequence 390
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US-09-331-204A-8
US-09-6472-928B-45
US-09-677-105-45
US-09-670-105-45
US-09-61-201-1935
US-10-061-201-1936
US-10-061-201-1936
US-09-0328-205-1935
US-09-328-205-1936
US-09-331-204-1
US-09-331-204-1
US-09-331-204-1
US-09-331-204A-4
US-09-331-204A-4
US-09-331-204A-6
US-10-310-188-38911
US-10-310-188-38912
US-10-310-188-38912
US-10-310-188-38913
US-10-310-188-6229
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Best Local Similarity
Matches 18; Conserv
      US-09-331-204A-7
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APPLICANT: Moncany, Maurice
APPLICANT: Montagnier, Luc
Montagnier, Luc
TITLE OF INVENTION: Nucleotide Sequences Derived From The
Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
And Their Uses In Particular For The Amplification Of The
Genomes Of These Retroviruses And For The In Vitro Diagnor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
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STATE: D.C.
COUNTRY: USAS

ZIP: 20005-3315

COMPUTER: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/670,105

FLING DATE: 26-Sep-2000

CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                          CURPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/472,928B
FILING APPLICATION THE TA:
APPLICATION NUMBER: US/08/465
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: RF 8912371
FILING DATE: 20-SEP-1989
PRIOR APPLICATION NUMBER: FR 8907354
APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
ATOMNEY AGENT INFORMATION:
NAME: MAYORY & KENNECH OF CENTER TO NUMBER: 25,146
REGISTRATION NUMBER: 20,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

85.6%; Score 15.4; DB 9;
Best Local Similarity 94.1%; Pred. No. 6.4e+04;
Matches 16; Conservative 0; Mismatches 1;
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APPLICATION NUMBER: 09/092,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-670-105-45; Sequence 45, Application US/09670105; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGAGGGGGAGGAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-472-928B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
"TWATH: 21 bear pairs
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STRANDEDNESS: single
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-05-331-204A-8

Sequence 8, Application US/09331204A

GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 18
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moncany, Maurice
APPLICANT: Moncany, Maurice
TITLE OF INVENTION: Use Comme of Retroviruses of The HIV-1, HIV-2 And SIV Type,
TITLE OF INVENTION: Genome of Retroviruses of The HIV-1, HIV-2 And SIV Type,
TITLE OF INVENTION: Genomes Of These Retroviruses And For The Amplification Of The
TITLE OF INVENTION: Of The Diseases Due To Those Viruses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: An oligomer; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic of OTHER INFORMATION: acid. This term includes oligomer's consisting of OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Dunner
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Pred. No. 2.7e+04;
0; Mismatches 1;
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  PCT/US97/23927
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PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 1997-12-19
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Best Local Similarity 94.4%;
Matches 17; Conservative (
                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: synthetic construct US-09-331-204A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 18
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US-08-472-928B-45
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ADDRESSEE:
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                                                                                                                                                                                                              FEATURE:
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                                                           Indels
                 Best Local Similarity 100.0%; Pred. No. 8.9e+04; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 45; 1
Pred. No. 8.9e+04;
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TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PRO178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT PILING DATE: 2002-01-30
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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US-10-061-201-1935/c

Sequence 1935, Application US/10061201

Sequence 1935, Application US/10061201

GENERAL INFORMATION:
APPLICANT: Shannon, Mark

TILLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REPERENCE: PB0178

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT PILING DATE: 2002-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR PE
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Best Local Similarity 100.0%; P. Matches 15; Conservative 0;
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                                                                                                                                        4 GAGGGGGAGGAGGGG
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CRGANISM: Homo sapiens
US-10-061-201-1935
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Llarity 94.1%; Pred. No. 6.4e+04;
Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meyers, Kenneth J.
REGIGTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0062-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCRMANION:
GENERAL INCRMANION:
TITLE OF INVERMANION:
HUMAN POSH-LIKE PROTEIN 1
FILE REPERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT APPLICATION NUMBER: DCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/472,928
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/160,465
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: FR 8912371
FILING DATE: 20-SEP-1989
APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-670-105-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TGGAGGGGGAGGGGG 18
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CRGANISM: Homo sapiens
US-10-061-201-1934
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Best Local Similarity
Matches 16; Conserva
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APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION WINBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
EBOOTH: 18
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GENERAL INFORMATION:
APPLICANT: ROSettedGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGILATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION UNMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFFWARE: Patentin version 3.1
SEQ ID NO 16894
LENGTH: 19
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Pred. No. 8.9e+04;
0; Mismatches 0;
                                                                                                                                    RESULT 13
US-60-328-205-1936/c
US-60-328-205-1936, Application US/60328205
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
ITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REPERENCE: AROMICA-26
CURRENT APPLICATION NUMBER: US/60/328,205
CURRENT APPLICATION NUMBER: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Acomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 6227, Application US/10310188; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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                              4 GAGGGGGAGGAGGGG 18
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Best Local Similarity 100.
Matches 15, Conservative
                                                                       16 GAGGGGGAGGAGGGG
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US-10-310-188-6227
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-60-328-205-1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-10-310-188-6227/c
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US-10-303-778-16894
                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1936
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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83.3%; Score 15; DB 87; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
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Pred. No. 8.9e+04;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             . 83.3%; Score 15; DB 45; I
y 100.0%; Pred, No. 8.9e+04;
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SEQUENCE 1935, Application US/60328205
SEQUENCE INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: AEOMICA-26
CURRENT PRILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE Aeomica Sequence Listing Engine
SEQ ID NO 1935
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: AEOMICA-26
CURRENT APPLICATION WIMBER: US/60/328,205
CURRENT FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1934
LENGTH: 17
PRIOR APPLICATION NUMBER: PCT/USG1/UGG63
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USG1/OG63
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-01-0
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1936
LENGTH: 17
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Second 28-205-1934/c
; Sequence 1934, Application US/60328205
; GENERAL INFORMATION:
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100.08; Fic
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Best Local Similarity 100.0%; Partches 15; Conservative 0;
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Best Local Similarity 100.
Matches 15, Conservative
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CORGANISM: Homo sapiens
US-60-328-205-1935
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CORGANISM: Homo sapiens
US-10-061-201-1936
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US-60-328-205-1934
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US-60-328-205-1935/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-16894

Query Match
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 3 GGAGGGGAGAGG 17

Db 4 GGAGGGAGAGGG 18

Search Completed: October 27, 2003, 17:52:53
Job time: 2356.29 secs
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Triplex forming ol CD28 inhibiting ph CD28 inhibition ol Nucleotide sequenc Nucleotide sequenc

Triplex forming ol CD28 inhibiting ph CD28 inhibition ol Hepatitis C virus

Hepatitis C virus
Triple helix formi
Human POSHLI scann
Human casein kinas
Gastric acid produ
TFO B13 sequence.
Human nuogo Hammerh
Human NOGO Hammerh
Human NOGO Inozyme
Human POSHLI scann
Human posHLI scann
Human tissue kalli
Hammerhead ribozym

Scoring table:

Searched:

Minimum DB Maximum DB

Database

score:

Title: Perfect :

Sequence:

OM nucleic

Run on:

Oestrogen receptor Human NOGO Hammerh Human NOGO Inozyme

Human Ets-2 phosph 3' flanking sequen Human psoriasis-li Human psoriasis-li Feline immunodefic

Human tissue kalli

us-09-331-204a-7.szlm22.rng

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Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; vixal disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD28 expression inhibiting oligonucleotide, RT05s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                          AAD03330
ABK00046
ABK00047
ABK00899
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ABV91219
ABV91225
AAV55680
AAF01954
AAF01954
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AAF16593
AAX32871
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AAA38350
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95US-0529878.
95US-0387041.
95US-0529878.
96WO-US01507
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(first entry)
09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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                                                                                                                                                            13.8
13.6
13.4
13.2
 AAT36242;
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AAT36242
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| SiD51/gcgdata/geneseqn-embl/NA1980.DAT:*
| SiD51/gcgdata/geneseqn-embl/NA1981.DAT:*
| SiD51/gcgdata/geneseqn-embl/NA1981.DAT:*
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| SiD51/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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| SiD51/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
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                                                                                   October 27, 2003, 10:32:29; Search time 162 Seconds (without alignments) 299.938 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                          2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
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AAX90335
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AAT98040
ABV91221
ABV91222
                                                            nucleic search, using sw model
                                                                                                                                                             ttggaggggaggagggg 18
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score greater than or equal to
and is derived by analysis of
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18
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seg length: 22
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Match
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16.4 15.4 15.4 15.4

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09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).
                                                                                                                                                                                                                                                                      Gaps
                                                                                                             The present oligonuclectide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral diseases, psoriasis type I diabetees mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, theumatorid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. stimulation of CD28 sporiasion may reduce the effects of antigenic in cytokine release
                                                                                                                                                                                                                                                                                                                                                                                                                                 CD28; inhibition; antisense oligonuclectide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                      gene expression in T cells - e.g. graft vs. host disease,
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                                                                                                                                                                                                                                                   Length 18,
                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                  100.0%; Score 18; DB 17; 100.0%; Pred. No. 5e+02;
                                                                                                                                                                                                                                Seguence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
                                                                                                                                                                                                             (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                      Mismatches
                                                                 for treating immune system diseases, septic shock, psoriasis, etc.
                                                        Oligo:nucleotide which reduces CD28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example, Column 24; 45pp; English.
                                                                                              Example 2; Page 45; 77pp; English.
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Best Local Similarity 10v...
Best Acade 18; Conservative
(ICNC ) ICN PHARM INC
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                                       WPI; 1996-384228/38
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                    Tam RC
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AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disease, eg. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple solerosis, uveitis, theumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic similation of CD28 positive T cells, with a consequent reduction in cycokine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reduction, T cell; CD28; gene expression; treatment; immune system disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoldes; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                          100.0%; Score 18; DB 20; Length 18; 100.0%; Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                   Mismatches
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95US-0529878.
95US-0387041.
95US-0529878.
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(first entry)
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                       present invention.
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amplification; gag; vpr; pol; vpu; HIV-1; HIV-2; SIV; nef2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This nucleotide sequence is found in posn. 6228-6208 of HIV-2 ROD and 6141-6121 of SIV-MAC. It is the anti-sense strand of a primer pair used to amplify these HIV-1, HIV-2 and SIV viral sequences, esp. in conjunction with in vitro diagnosis of infection. It is useful for treating viral diseases, eg. AIDS. See also AAO06905-31 and AAO06933-54 (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                            New nucleotide sequences derived from genome of HIV-1, HIV-2 and SIV - useful as primers for amplification of immuno-deficiency viruses in diagnosis and for raising antibodies in treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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    MM\gamma24 nucleotide constituent of vpx gene of HIV-2 ROD and SIV-MAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.4; DB 11;
Pred. No. 4.5e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 5 A; 2 C; 13 G; 1 T; 0 other;
                                                        HIV-2; SIV; AIDS; anti-sense nucleotide; ss
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; page 20; 24pp; French
                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR.
(INRM ) INSERM INST NAT SANTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
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                                                                                                    Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.6%;
94.1%;
                                                                                      Human immunodeficiency virus
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                                                                                                                                                                                                                          89FR-0012371.
                                                                                                                                                                                              90EP-0401520
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(first entry)
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vif2; vpx; detection; ss.
                                                                                                                                                                                                                                                                                                      Montagnier
                                                                                                                                                                                                                                                                                                                                  WPI; 1990-378039/51.
                                                                                                                                                                                                                                                                                                                                                                                                            HIV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1990;
                                                                                                                                                                                              05-JUN-1990;
                                                                                                                                                                                                                           20-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
08-SEP-1998
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                                                                                                                                                               19-DEC-1990
                                                                                                                                  EP403333-A.
                                                                                                                                                                                                                                                                                                      Moncany M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT98040;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                           Gaps
                                                                                                                                                                                                                                                                                                      CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
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              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                          Indels
                                                                                                                                                                                                                                                                       CD28 inhibiting phosphorothioate oligonucleotide RT09S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.4; DB 20;
Pred. No. 2e+03;
0; Mismatches 1;
             Score 16.4; DB 17;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
                                          Mismatches
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94.4%;
           91.1%;
ilarity 94.4%;
Conservative
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                                                                         1 TTGGAGGGGGAGGAGGGG
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                                                                                                                                                                               AAX90336 standard; DNA; 18
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(first entry)
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                                                                                                                                                                                                                                                                                                                                     phosphorothioate; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-443609/37
           Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                          24-SEP-1999
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05-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                               US5932556-A.
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                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Best Loca Matches

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AAQ06932 RESULT

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Gaps

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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (S1, haring 95% deviations, especially of Sequence identity to (S1), (S1), and post in the sequence having 55% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Chuman POSHL 1 is a prote-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as CC downstream components of the signal transduction pathway. (I) is useful considering theoretic binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating concert, they useful for diagnosing, monitoring disease and treating concert, they useful in the development of vaccines and (II) is useful for measuring and for surveying gene expression and creating create sequence is that of a scanning oligonucleotide useful in examples of present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, POSHL 1, SH3 domain, POSH-like signalling protein 1, oncogene; Rho GTPase, signal transduction, gene expression, cancer, vaccine;
                                                                    Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1 -
                                                                                                                              Example 2; SEQ ID NO 1934; 60pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.3%; Score 15; DB 24; Length 17; 100.0%; Pred. No. 6.5e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human POSHL1 scanning oligonucleotide SEQ 1D NO 1935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 1 A; 12 C; 0 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001MO-US006665.
30-JAN-2001; 2001MO-US00666.
30-JAN-2001; 2001MO-US00667.
30-JAN-2001; 2001MO-US00669.
30-JAN-2001; 2001MO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; transgenic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GAGGGGGAGGAGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-2002; 2002EP-0001165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGGGGAGGAGGGG 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 15; Conservative
                                        WPI; 2002-684061/74.
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             Shannon M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV91222;
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ID ABV912
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                                                                                                                                                                                                                                                                 The oligonuclectides AAT98010-T98059 are useful as primers for nucleic acid amplification of conserved sequences of the gag, vpr, pol or vpu genes of the HTV-1 strains Bru, Mal, Eli, HTV-2 RDD or simian immunodeficiency virus (SIV) MAC or the nef2, vif2 or vpx genes of HTV-2 RDD and SIV MAC. This primer is targetted to sequences in the vpx gene of HTV-2 or SIV infections.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
Rho GTPase; signal transduction; gene expression; cancer; vaccine;
gene therapy; transgenic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                              Oligo-nucleotide primers for amplifying retroviral nucleic acids - comprising conserved sequences of human immunodeficiency virus and simian immunodeficiency virus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.4; DB 18;
Pred. No. 4.5e+03;
0; Mismatches 1;
                                                                    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 5 A; 2 C; 13 G; 1 T; 0 other;
                                                                                                                                                                                                                                        Claim 10; Page 21; 23pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAGGGGAGGAGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TGGAGGGGGAGGAG 19
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2001WO-US00668.
2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.6%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US00663.
2001WO-US00664.
2001WO-US00665.
           89FR-0007354.
89FR-0012371.
90EP-0401520.
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10-0CT-2001; 2001US-0328205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00670
23-MAY-2001; 2001US-0864761
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Query Match

Best Local Similarity 94.1,",

Best 16, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                     Moncany M, Montagnier L;
                                                                                                                                                WPI; 1997-538622/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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30-JAN-2001;
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                           20-SEP-1989;
05-JUN-1990;
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             02-JUN-1989;
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ABV91221/c
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Gaps

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English

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The invention relates to an isolated SH3 domain (POSH) like signalling protein 1 (POSH1 1) polypeptide (1) comprising a sequence of 730 amino acids (SI, ABBA3999), a sequence having 65$ sequence identity to (SI), (SI) having 95$ deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSH1 is a prote-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating caused by altered expression of human POSH1 including diagnosing and creating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating create sequence is that of a scanning oligonucleotide useful in examples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, POSHL 1, SH3 domain, POSH-like signalling protein 1, oncogene, Rho GPPase, signal transduction, gene expression, cancer, vaccine, gene therapy, transgenic; ss.
                                                                                                                                                        Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human POSHL1 scanning oligonucleotide SEQ ID NO 1936.
                                                                                                                                                                                                                                      Example 2; SEQ ID NO 1935; 60pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 24; L
Pred. No. 6.5e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 1 A; 12 C; 0 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%; Scc...
100.0%; Pre
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30-JAN-2001; 2001WO-US00664.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00666.
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23-MAY-2001; 2001US-0864761.
10-OCT-2001; 2001US-0328205.
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                                                                                                                       WPI; 2002-684061/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 15; Conserv
                                                    (AEOM-) AEOMICA INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-2002.
                                                                                       Shannon M;
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0; Gaps

Length 17; 0; Indels

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The invention relates to an isolated SH3 domain (POSH)-like signalling cortes (1) polypeptide (1) comprising a sequence of 730 amino acids (21, ABBA399), a sequence having 65% sequence identity to (81), and to sequence having 65% sequence identity to (81), a sequence comprising at least 8 contiguous amino acids. Finament of the sequences comprising at least 8 contiguous amino acids. CC fragment protein that interacts with Rho family small GTPases as well as adaptor protein that interacts with Rho family small GTPases as well as consistent components of the signal transduction pathway. (1) is usseful controlled in a particular signal transduction pathway. (1) is usseful considered by altered expression of human POSH11 including disease and treating caused by altered expression of human POSH11 including disease and treating caused by useful in the development of vaccines and (11) is useful for measuring and for surveying gene expression and creating creating that of a scanning objection to the proteins. The present sequence is that of a scanning objective that the constructing the proteins. The minimals capable of producing the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                 Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'.UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'.untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 1936; 60pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%; Score 15; DB 24; L
100.0%; Pred. No. 6.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 1 A; 12 C; 1 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
2001WO-US00669.
2001WO-US00669.
2001WO-US00669.
2001WO-US00670.
2001US-0864761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GAGGGGGAGGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT36196 standard; DNA; 18
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
es 15; Conservative
                                                                                                                                                                                                    WPI; 2002-684061/74.
                                                                                                                             (AEOM-) AEOMICA INC.
 30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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15-APR-1997
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                                                                       23-MAY-2001;
10-OCT-2001;
                                                                                                                                                                 Shannon M;
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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90289 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                 The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8 \,
Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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                                                                                                                                                                                                                                                                       Score 14.8; DB 20;
Pred. No. 7.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
                                                                                                                                                                                                                                                     Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD28 inhibition oligonucleotide RT03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Column 29; 45pp; English.
                                                      Example; Column 21; 45pp; English
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                                                                                                                                                                                                                                                                                          82.2%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-443609/37
                                                                                                                                                                                                                      present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                              The present oligonuclectide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, partiasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                                                                                                                                                                                 for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%; Score 14.8; DB 17; Length 18; 88.9%; Pred. No. 7.6e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD28 inhibiting phosphorothioate oligonucleotide RT03S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 54; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTGGAGGGGGAGGGG 18
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                                                                      95US-0387041.
95US-0529878.
95US-0387041.
95US-0529878.
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                                     96WO-US01507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                               (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-443609/37
                                                                                                                                                                                                                                       WPI; 1996-384228/38.
                                                                      09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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                                     05-FEB-1996;
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 15-AUG-1996
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Matches
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rrdcaddeddrddrdddd 18

AAZ99625

AAZ99625 standard; DNA; 18 AAZ99625;

Nucleotide sequence of G-motif oligonucleotide GR1

12-JUL-2000 (first entry)

G-motif oligonucleotide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation, natural Killer cell; septic shock; cytotoxic T-lymphocyte, inflammation, autoimmune disease, rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple sclerosis; Kawasaki syndrome; graft-versus-host disease, transplant rejection, helper T cell response 1-mediated disease, Lyme arthritis, streptococcal induced arthritis, chronic inflammatory bowel disease; psoriasis vulgaris, experimental allergic encephalomyclitis, insulin-dependent diabetes mellitus, bacterial infection; tumour; ss.

Synthetic.

WO200014217-A2.

16-MAR-2000

99WO-EP06502 03-SEP-1999;

(CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

Heeg K; Wagner H, Lipford GB,

WPI; 2000-256970/22.

Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -

Example 14; Page 32; 75pp; English

The present sequence represents a G-motif oligonuclectide of the invention. The specification describes compositions comprising G-motif oligonuclectides inhibit activation of antigenuclectides. The G-motif oligonuclectides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonuclectides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arrhitis, Crohn's disease, sarciodosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell response 1-mediated cliseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflections, parasitic inflections (e.g. Leishmaniasis or Toxoplasmosis), viral infections, parasitic inflections (e.g. Cytomegalovirus and human immunodeficiency viral infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage

Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Gaps ·, Length 18; Indels Score 14.8; DB 21; Pred. No. 7.6e+03; 0; Mismatches 2; 82.2%; Query Match
Best Local Similarity 88.9
Matches 16; Conservative

1 TTGGAGGGGTGGTGGGG 18

RESULT 14 AAZ99650/

AAZ99650 standard; DNA; 18 BP

AAZ99650;

12-JUL-2000 (first entry)

Nucleotide seguence of non-G-motif oligonucleotide GRFlcomp.

G-motif oligonucleotide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation, natural killer cell; septic shock; cytotoxic T-lymphocyre, inflammation, autoimmune disease; rheumatoxi arthritis; Crohn's disease, sarcoidosis; multiple sclerosis; Kawasaki syndrome, graft-versus-host disease, transplant rejection; helper T cell response 1 mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

Synthetic.

WO200014217-A2

16-MAR-2000.

99WO-EP06502. 03-SEP-1999;

98EP-0116652, 03-SEP-1998;

(CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

Heeg K; Lipford GB, Wagner H,

WPI; 2000-256970/22.

Compositions comprising G-motif oligonucleotides useful for e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections

Example 14; Page 32; 75pp; English.

The present sequence represents a non-G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides. The G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic configurations of vaccines for treatment of configurations of vaccines for treatment seed for the productions of vaccines for treatment seed for the productions of vaccines for treatment seed for the sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell response 1-mediated disease (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic infections, and insulin-dependent diabetes mellitus), baccerial corephalomyelitis, and insulin-dependent diabetes mellitus), baccerial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage

Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

Gaps . 0 Length 18; Indels 82.2%; Score 14.8; DB 21; 88.9%; Pred. No. 7.69+03; Mismatches 2; Conservative Best Local Similarity Matches 16; Conserv Query Match

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Reduction, T cell, CD28, gene expression, treatment, immune system, disorder, graft versus host disease, septic shock, viral disease, postriasis, type I diabetes mellitus, thyrolditis, sarcoides, multiple sclerosis, uvetis; rhelmatoid arthritis, 5-UTR, systemic lupus erythematosus, inflammatory bowel disease, triplex forming, oligonucleotide, 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, posniasis, type I diabetes mallitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-WAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                    Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 54; 77pp; English.
18 TTGGAGGGGTGGTGGGG 1
                                                                                            AAT36197 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0387041.
95US-0529878.
95US-0387041.
95US-0529878.
                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US01507
                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ICNC ) ICN PHARM INC.
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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15-APR-1997
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                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                        AAT36197;
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                                                             RESULT 15
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Query Match

82.2%; Score 14.8; DB 17; Length 21;

Bet Local Similarity 88.9%; Pred. No. 7.66+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0;

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Gaps

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Search completed: October 27, 2003, 11:25:20 Job time : 163 secs

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Lipford,G.B., Heeg,K. and Magner,H.
G-morif oligonucleotides and uses thereof
Parent: WO 0014217-A 17 16-MAR-2000,
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE)
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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20gence 17 from Patent WO0014217.
AX023402
AX023402.1 GI:10183802
                                                                 SUMMARIES
                                                                                                                                                                           AX023402

AX023417

AX102447

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                       GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            nucleic search, using sw model
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AX03427 Sequence
AX131393 Sequence
BX0101798 Immunogen
AX52426 Sequence
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AX52426 Sequence
AX52427 Sequence
AX52429 Sequence
AX65035 Sequence
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AX14603 Sequence
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AX21463 Sequence
AX12673 Sequence
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AX5267 Sequence
AX5267 Sequence
AX668 Nucleotide
AX668 Nucleotide

PAT 15-SEP-2000

linear

AKO88921 Sequence AK152368 Sequence AK012712 Sequence AK0186922 Sequence AK152369 Sequence AK152369 Sequence AK23303 Sequence AK23303 Sequence AK234383 Antisense BD138139 Antisense

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Moncany, M. and Montagnier, L.
Moncany, M. and Montagnier, L.
Nuclectide sequences derived from the genome of retroviruses of the HIV-1, HIV-2, and SIV type, and their uses in particular for the amplification of the genomes of these retroviruses and for the in vitro diagnosis of the diseases due to these viruses
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/db_xref="taxon:32630"
/note="Antisense Oligonucleotide"
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Pred. No. 2.6e+05;
0; Mismatches 2;
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76.7%; Score 13.8; DB 6;
Best Local Similarity 88.2%; Pred, No. 2.5e+05;
Matches 15; Conservative 0; Mismatches 2;
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/mol type="genomic DNA"
/db_Xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipford, G.B., Heeg, K. and Magner, H.
G-morif oligonucleotides and uses thereof
Patent: WO 01417-A 42 16-WAR-2000;
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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/organism="synthetic construct"
/mol_type="genomic DN"
/db_xref="taxon:32630"
/note="synthetic, no natural origin"
                                             1. 18
/organism="synthetic construct"
/mol type="genomic DNA"
/db xref="taxon:32630"
/noTe="synthetic, no natural origin"
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Pred. No. 2.4e+04;
0; Mismatches 1;

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/organism="synthetic construct"
/mol_type="genomic DNA"

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Sequence 174 from Patent WO0210378.
AX418779
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Sequence 42 from Patent WO0014217.
AX023427
AX023427.1 GI:10183827
    CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 4e+05;
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Patent: EP 1239051-A 1935 11-SEP-2002;
Aeomica, Inc. (US)
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Patent: BP 1239051-A 1936 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 1935 from Patent EP1239051.
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              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
12 c 0 9
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AX532427/c
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INST PASSEUR. INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL
OS Artificial Sequence
NN UP 2000093187-A/45
PP 24-SEP-1999 UP 1999270165
PR 24-SEP-1999 UP 1999270165
PR 02-UTN-1989 FR 89/0234,20-SEP-1989 FR 89/12371 PI
MAURICE MONCANY, LUC MONTANIER 800,0384,20-SEP-1989 FR 89/12371 PI
PC C12N15/09,A61K39/21,A61K48/00,A61P31/18,C07H21/04,C07K14/155,
PC C12Q1/68,C12Q1/70,G1N33/569,C12N15/00
CC C07K14/16,
PC C12Q1/68,C12Q1/70,G1N33/569,C12N15/00
CC T12Q1/68,C12Q1/70,G1N33/569,C12N15/00
CC T12Q1/68,C12Q1/70,G1N33/569,C12N15/00
CC T12Q1/68,C12Q1/70,G1N33/569,C12N15/00
FFH Key Location/Qualifiers
FFT Source //organism='Artificial Sequence'.
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                                                                                                                                                    BD001798 21-JAN-2002
Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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BD001798.1 GI.18626357

BD001798.1 GI.18626357

D 2000093187-A/45.

Synthetic construct

artificial sequences.

I (bases I to 21)

Moncany, m, and Montagnier, L.

Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2.
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/organism='Artificial Sequence'
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Pred. No. 2.6e+05;
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                  Indels
Pred. No. 2.6e+05;
); Mismatches 2;
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/organism="synthetic construct"
/mol_type="genomic DNN"
/db_xref="taxon:32630"
db_z c 13 g 1 t
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Patent: EP 1239051-A 1934 11-SEP-2002;
Aeomica, Inc. (US)
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AX532425
AX532425.1 GI:25256625
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Homo sapiens
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Best Local Similarity 88.2
Matches 15; Conservative
Best Local Similarity
Matches 15, Conserv
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Sequence 9409 from patent US 6537751.
AR297674
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1 (bases 1 to 19)
Watanabe,K.A., Ren,W.-Y. and Weil,R.
Complementary DNA and toxins
Patent: US 5652350-A 37 29-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                     (bases 1 to 19)
Watenabe, K.A., Ren, W.-Y. and Weil, R.
Complementary DNA and toxins
Patent: US 5571937-A 37 05-NOV-1996;
Location/Qualifiers
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Sequence 37 from patent US 5652350.
158746
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Sequence 37 from patent US 5571937.
128584
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1 0 c 12 g
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1 (bases 1 to 20)
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 Length 17;
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Thf-inducible promoters and methods for using Patent: WO 0246433-A 67 13-JUN-2002; Saus, Juan (ES)
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1.19
| Organism="synthetic construct" | /organism="synthetic construct" | /mol_type="genomic DNA" | /db_xref="texon:32630" | /noTe="Primer ON-DHFR-F1"
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/mol_type="genomic DNA"
/db_xref="taxon:32650"
/note="Primer ON-DHFR-F1"
3 a 2 c 11 g 3 t
Score 13.4; DB 6;
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Best Local Similarity 93.3%; Pred. No. 3.9e+05;
Matches 14; Conservative 0; Mismatches 1;
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Patent: WO 0246378-A 67 13-JUN-2002;
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Sequence 67 from Patent W00246433.
AX477615
AX477615.1 GI:22216795
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Sequence 67 from Patent W00246378.
AX505035
AX505035.1. GI:23386357
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="Antisense PCR primer for CC3 promoter (spec Table IIIa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poole, J., Roninson, I.B. and Chang, B.D.
Reagents and methods for identifying and modulating expression of genes regulated by cdk inhibitors
Patent: WO 02066681-A 22 29-AUG-2002;
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 637751-A 9409 25-MAR-2003;
Location/Qualifiers
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74.4%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels
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Sequence 22 from Patent W002066681.
AX662935.1 GI:29163516
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|organism="unknown"
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